

# SEQUENCE LISTING

<110> Brugliera, Filippa  
Holton, Timothy A.  
Michael, Michael Z.

<120> GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES  
AND USES THEREFOR

<130> 11658

<140> 09/142,108

<141> 1998-09-01

<150> PN8386

<151> 1996-03-01

<160> 45

<170> PatentIn Ver. 2.1

<210> 1

<211> 1789

<212> DNA

<213> Petunia x hybrida

<220>

<221> CDS

<222> (50)..(1588)

<400> 1

gcaggaattg gtgaacccca tagaagtaaa atactcctat ctttatttc atg gaa atc 58  
Met Glu Ile  
1

tta agc cta att ctg tac acc gtc att ttc tca ttt ctt cta caa ttc 106  
Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe  
5 10 15

att ctt aga tca ttt ttc cgt aaa cgt tac cct tta cca tta cca cca 154  
Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro  
20 25 30 35

ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202  
Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro  
40 45 50

aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250  
Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu  
55 60 65

atg tat ctt aag atg ggg ttc gta gac gtg gtg gtt gca gcc tcg gca 298  
Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser Ala  
70 75 80

tcg gtt gca gct cag ttc ttg aaa act cat gat gct aat ttc tcg agc 346

Ser	Val	Ala	Ala	Gln	Phe	Leu	Lys	Thr	His	Asp	Ala	Asn	Phe	Ser	Ser		
85						90					95						
cgt	cca	cca	aat	tct	ggt	gca	gaa	cat	atg	gct	tat	aat	tat	cag	gat	394	
Arg	Pro	Pro	Asn	Ser	Gly	Ala	Glu	His	Met	Ala	Tyr	Asn	Tyr	Gln	Asp		
100					105					110					115		
ctt	gtt	ttt	gca	cct	tat	gga	cct	aga	tgg	cgt	atg	ctt	agg	aaa	att	442	
Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Leu	Arg	Lys	Ile		
				120					125					130			
tgc	tca	gtt	cac	ctt	ttc	tct	acc	aag	gct	tta	gat	gac	ttc	cgc	cat	490	
Cys	Ser	Val	His	Leu	Phe	Ser	Thr	Lys	Ala	Leu	Asp	Asp	Phe	Arg	His		
			135					140					145				
gtc	cgc	cag	gat	gaa	gtg	aaa	aca	ctg	acg	cgc	gca	cta	gca	agt	gca	538	
Val	Arg	Gln	Asp	Glu	Val	Lys	Thr	Leu	Thr	Arg	Ala	Leu	Ala	Ser	Ala		
		150					155					160					
ggc	caa	aag	cca	gtc	aaa	tta	ggt	cag	tta	ttg	aac	gtg	tgc	acg	acg	586	
Gly	Gln	Lys	Pro	Val	Lys	Leu	Gly	Gln	Leu	Leu	Asn	Val	Cys	Thr	Thr		
	165					170					175						
aac	gca	ctc	gcg	cga	gta	atg	cta	ggt	aag	cga	gta	ttt	gcc	gac	gga	634	
Asn	Ala	Leu	Ala	Arg	Val	Met	Leu	Gly	Lys	Arg	Val	Phe	Ala	Asp	Gly		
180					185					190					195		
agt	ggc	gat	gtt	gat	cca	caa	gcg	gcg	gag	ttc	aag	tca	atg	gtg	gtg	682	
Ser	Gly	Asp	Val	Asp	Pro	Gln	Ala	Ala	Glu	Phe	Lys	Ser	Met	Val	Val		
				200					205					210			
gaa	atg	atg	gta	gtc	gcc	ggt	gtt	ttt	aac	att	ggt	gat	ttt	att	ccg	730	
Glu	Met	Met	Val	Val	Ala	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro		
			215				220						225				
caa	ctt	aat	tgg	tta	gat	att	caa	ggt	gta	gcc	gct	aaa	atg	aag	aag	778	
Gln	Leu	Asn	Trp	Leu	Asp	Ile	Gln	Gly	Val	Ala	Ala	Lys	Met	Lys	Lys		
		230					235					240					
ctc	cac	gcg	cgt	ttc	gac	gcg	ttc	ttg	act	gat	ata	ctt	gaa	gag	cat	826	
Leu	His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Thr	Asp	Ile	Leu	Glu	Glu	His		
	245					250					255						
aag	ggt	aaa	att	ttt	gga	gaa	atg	aaa	gat	ttg	ttg	agt	act	ttg	atc	874	
Lys	Gly	Lys	Ile	Phe	Gly	Glu	Met	Lys	Asp	Leu	Leu	Ser	Thr	Leu	Ile		
260					265					270					275		
tct	ctt	aaa	aat	gat	gat	gcg	gat	aat	gat	gga	ggg	aaa	ctc	act	gat	922	
Ser	Leu	Lys	Asn	Asp	Asp	Ala	Asp	Asn	Asp	Gly	Gly	Lys	Leu	Thr	Asp		
				280					285					290			
aca	gaa	att	aaa	gca	tta	ctt	ttg	aac	ttg	ttt	gta	gct	gga	aca	gac	970	
Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Val	Ala	Gly	Thr	Asp		
			295				300						305				
aca	tct	tct	agt	aca	gtt	gaa	tgg	gcc	att	gct	gag	ctt	att	cgt	aat	1018	

Thr	Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg	Asn	
		310					315					320				
cca	aaa	ata	cta	gcc	caa	gcc	cag	caa	gag	atc	gac	aaa	gtc	gtt	gga	1066
Pro	Lys	Ile	Leu	Ala	Gln	Ala	Gln	Gln	Glu	Ile	Asp	Lys	Val	Val	Gly	
	325					330					335					
agg	gac	cgg	cta	gtt	ggc	gaa	ttg	gac	cta	gcc	caa	ttg	aca	tac	ttg	1114
Arg	Asp	Arg	Leu	Val	Gly	Glu	Leu	Asp	Leu	Ala	Gln	Leu	Thr	Tyr	Leu	
	340				345					350					355	
gaa	gct	ata	gtc	aag	gaa	acc	ttt	cgg	ctt	cat	cca	tca	acc	cct	ctt	1162
Glu	Ala	Ile	Val	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	
				360					365						370	
tca	ctt	cct	aga	att	gca	tct	gag	agt	tgt	gag	atc	aat	ggc	tat	ttc	1210
Ser	Leu	Pro	Arg	Ile	Ala	Ser	Glu	Ser	Cys	Glu	Ile	Asn	Gly	Tyr	Phe	
			375					380								
att	cca	aaa	ggc	tca	acg	ctt	ctc	ctt	aat	gtt	tgg	gcc	att	gct	cgt	1258
Ile	Pro	Lys	Gly	Ser	Thr	Leu	Leu	Leu	Asn	Val	Trp	Ala	Ile	Ala	Arg	
		390					395					400				
gat	cca	aat	gca	tgg	gct	gat	cca	ttg	gag	ttt	agg	cct	gaa	agg	ttt	1306
Asp	Pro	Asn	Ala	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	
	405					410					415					
ttg	cca	gga	ggt	gag	aag	ccc	aaa	gtt	gat	gtc	cgt	ggg	aat	gac	ttt	1354
Leu	Pro	Gly	Gly	Glu	Lys	Pro	Lys	Val	Asp	Val	Arg	Gly	Asn	Asp	Phe	
	420				425					430					435	
gaa	gtc	ata	cca	ttt	gga	gct	gga	cgt	agg	att	tgt	gct	gga	atg	aat	1402
Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Asn	
				440					445						450	
ttg	ggt	ata	cgt	atg	gtc	cag	ttg	atg	att	gca	act	tta	ata	cat	gca	1450
Leu	Gly	Ile	Arg	Met	Val	Gln	Leu	Met	Ile	Ala	Thr	Leu	Ile	His	Ala	
			455					460							465	
ttt	aac	tgg	gat	ttg	gtc	agt	gga	caa	ttg	ccg	gag	atg	ttg	aat	atg	1498
Phe	Asn	Trp	Asp	Leu	Val	Ser	Gly	Gln	Leu	Pro	Glu	Met	Leu	Asn	Met	
		470					475					480				
gaa	gaa	gca	tat	ggg	ctg	acc	tta	caa	cgg	gct	gat	cca	ttg	gtt	gtg	1546
Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Asp	Pro	Leu	Val	Val	
	485					490					495					
cac	cca	agg	cct	cgc	tta	gaa	gcc	caa	gcg	tac	att	ggg	tga			1588
His	Pro	Arg	Pro	Arg	Leu	Glu	Ala	Gln	Ala	Tyr	Ile	Gly				
	500				505					510						
gcagcaacag cccatggaga taacatgagt gttaaagtga tgagtctcca tatcttgttt																1648
agtttgttta tgctttggat ttagtagttt ttatattgat agatcaatgt ttgcattgtc																1708
agtaagaata tccgttgctt gtttcattaa ctccaggtgg acaataaaaag aagtaatttg																1768

tatgaaaaaa aaaaaaaaaa a

1789

<210> 2  
<211> 512  
<212> PRT  
<213> Petunia x hybrida

<400> 2  
Met Glu Ile Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu  
1 5 10 15  
Leu Gln Phe Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro  
20 25 30  
Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His  
35 40 45  
Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr  
50 55 60  
Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala  
65 70 75 80  
Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn  
85 90 95  
Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn  
100 105 110  
Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu  
115 120 125  
Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp  
130 135 140  
Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu  
145 150 155 160  
Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val  
165 170 175  
Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe  
180 185 190  
Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser  
195 200 205  
Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp  
210 215 220  
Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys  
225 230 235 240  
Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu  
245 250 255  
Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser  
260 265 270  
Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys  
275 280 285  
Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala  
290 295 300  
Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu  
305 310 315 320  
Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys  
325 330 335  
Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu  
340 345 350  
Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser  
355 360 365

Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn  
 370 375 380  
 Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala  
 385 390 395 400  
 Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro  
 405 410 415  
 Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly  
 420 425 430  
 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala  
 435 440 445  
 Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu  
 450 455 460  
 Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met  
 465 470 475 480  
 Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro  
 485 490 495  
  
 Leu Val Val His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly  
 500 505 510

<210> 3  
 <211> 1745  
 <212> DNA  
 <213> *Dianthus caryophyllus*

<220>  
 <221> CDS  
 <222> (172)..(1662)

<400> 3  
 aagttcggca cgagcgtcac attcacaccg tcacattact attcaaacca ctcattttct 60  
 acctctcttt tctaccacc aaaacaaaac aaaacaaaaa aaaacacata aaaaaactca 120  
 aaaaaaatt ataatgtcac ccttagaggt aactttctac accatagtc t atg cac 177  
 Met His  
 1  
  
 aat ctc tac tac ctc atc acc acc gtc ttc cgc ggc cac caa aaa ccg 225  
 Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro  
 5 10 15  
  
 ctt cct cca ggg cca cga cca tgg ccc atc gtg gga aac ctc cca cat 273  
 Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His  
 20 25 30  
  
 atg ggc cag gca ccg cac cag ggc tta gca gcc ctg gcg caa aag tat 321  
 Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr  
 35 40 45 50  
  
 ggc cct cta ttg tat atg aga ctg ggg tac gtg gac gtt gtt gtg gcc 369  
 Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val Val Ala  
 55 60 65  
  
 gcc tca gcg tct gta gcg acc cag ttt ctt aag aca cat gac cta aat 417

Ala	Ser	Ala	Ser	Val	Ala	Thr	Gln	Phe	Leu	Lys	Thr	His	Asp	Leu	Asn	
			70					75					80			
ttt	tcg	agt	agg	cca	ccg	aat	tcg	ggg	gct	aaa	cac	att	gct	tat	aac	465
Phe	Ser	Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Ile	Ala	Tyr	Asn	
		85					90					95				
tat	caa	gac	ctt	gtt	ttt	gca	cct	tat	gga	cct	aaa	tgg	cgc	atg	ctt	513
Tyr	Gln	Asp	Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Lys	Trp	Arg	Met	Leu	
	100					105					110					
agg	aaa	att	tgt	tcc	tta	cac	atg	ttt	tct	tct	aag	gct	ttg	gac	gat	561
Arg	Lys	Ile	Cys	Ser	Leu	His	Met	Phe	Ser	Ser	Lys	Ala	Leu	Asp	Asp	
115					120					125					130	
ttt	aga	ctt	gtc	cgt	cag	gaa	gaa	gta	tct	ata	ctg	gta	aat	gcg	ata	609
Phe	Arg	Leu	Val	Arg	Gln	Glu	Glu	Val	Ser	Ile	Leu	Val	Asn	Ala	Ile	
				135					140					145		
gca	aaa	gca	gga	aca	aag	cca	gta	caa	cta	gga	caa	cta	ctc	aac	gtg	657
Ala	Lys	Ala	Gly	Thr	Lys	Pro	Val	Gln	Leu	Gly	Gln	Leu	Leu	Asn	Val	
			150					155						160		
tgc	acc	aca	aat	gcc	tta	tcg	agg	gtg	atg	cta	ggg	aag	cga	gtt	ctc	705
Cys	Thr	Thr	Asn	Ala	Leu	Ser	Arg	Val	Met	Leu	Gly	Lys	Arg	Val	Leu	
		165					170					175				
ggg	gat	ggc	aca	ggg	aaa	agc	gac	cca	aaa	gcc	gag	gaa	ttt	aag	gac	753
Gly	Asp	Gly	Thr	Gly	Lys	Ser	Asp	Pro	Lys	Ala	Glu	Glu	Phe	Lys	Asp	
	180					185					190					
atg	gtg	ctg	gag	tta	atg	gtt	ctc	acc	gga	gtt	ttt	aac	att	ggc	gat	801
Met	Val	Leu	Glu	Leu	Met	Val	Leu	Thr	Gly	Val	Phe	Asn	Ile	Gly	Asp	
195					200					205					210	
ttt	gta	ccg	gca	ttg	gaa	tgt	cta	gac	tta	caa	ggg	gtt	gca	tct	aaa	849
Phe	Val	Pro	Ala	Leu	Glu	Cys	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	
				215					220					225		
atg	aag	aaa	tta	cat	aaa	aga	ctt	gat	aat	ttt	atg	agt	aac	att	ttg	897
Met	Lys	Lys	Leu	His	Lys	Arg	Leu	Asp	Asn	Phe	Met	Ser	Asn	Ile	Leu	
			230					235						240		
gag	gaa	cac	aag	agt	gtt	gca	cat	caa	caa	aat	ggg	gga	gat	ttg	cta	945
Glu	Glu	His	Lys	Ser	Val	Ala	His	Gln	Gln	Asn	Gly	Gly	Asp	Leu	Leu	
		245					250					255				
agc	att	ttg	ata	tct	ttg	aag	gat	aat	tgt	gat	ggg	gaa	ggg	ggc	aag	993
Ser	Ile	Leu	Ile	Ser	Leu	Lys	Asp	Asn	Cys	Asp	Gly	Glu	Gly	Gly	Lys	
	260					265					270					
ttt	agt	gcc	aca	gaa	att	aag	gcc	ttg	cta	ttg	gat	tta	ttt	aca	gct	1041
Phe	Ser	Ala	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asp	Leu	Phe	Thr	Ala	
275					280					285					290	
gga	aca	gac	aca	tca	tct	agt	aca	act	gaa	tgg	gcc	ata	gcc	gaa	cta	1089

Gly Thr Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala Glu Leu	
295 300 305	
att cgc cat cca aaa atc tta gcc caa gtt caa caa gaa atg gac tca	1137
Ile Arg His Pro Lys Ile Leu Ala Gln Val Gln Gln Glu Met Asp Ser	
310 315 320	
gtc gtg ggc cga gac cga ctc ata gcc gaa gct gac ata ccg aac cta	1185
Val Val Gly Arg Asp Arg Leu Ile Ala Glu Ala Asp Ile Pro Asn Leu	
325 330 335	
acc tac ttc caa gcc gta atc aaa gag gtt ttc cga ctt cac ccg tcc	1233
Thr Tyr Phe Gln Ala Val Ile Lys Glu Val Phe Arg Leu His Pro Ser	
340 345 350	
acc ccg ctt tcc cta cca cgg gtc gca aac gaa tcg tgc gaa ata aac	1281
Thr Pro Leu Ser Leu Pro Arg Val Ala Asn Glu Ser Cys Glu Ile Asn	
355 360 365 370	
ggg tac cac att ccc aaa aac acc act tta ttg gta aat gtg tgg gcc	1329
Gly Tyr His Ile Pro Lys Asn Thr Thr Leu Leu Val Asn Val Trp Ala	
375 380 385	
atc gca cgc gac cct gag gtt tgg gcc gac ccg tta gag ttt aaa ccc	1377
Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe Lys Pro	
390 395 400	
gaa aga ttt ttg ccg ggc ggc gaa aag ccc aat gtg gat gtg aaa gga	1425
Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly	
405 410 415	
aac gat ttt gag ctg att ccg ttc ggg gcg ggc cga ccg att tgt gct	1473
Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala	
420 425 430	
ggg ctg agt ttg ggc ctg cgt atg gtc cag ttg atg aca gcc act ttg	1521
Gly Leu Ser Leu Gly Leu Arg Met Val Gln Leu Met Thr Ala Thr Leu	
435 440 445 450	
gcc cat act tat gat tgg gcc tta gct gat ggg ctt atg ccc gaa aag	1569
Ala His Thr Tyr Asp Trp Ala Leu Ala Asp Gly Leu Met Pro Glu Lys	
455 460 465	
ctt aac atg gat gag gct tat ggg ctt acc tta cag cgt aag gtg cca	1617
Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Lys Val Pro	
470 475 480	
ctt aat ggt cca ccc gac ccc gtc ggc ttc tcg gcc cgt gtt taa	1662
Leu Asn Gly Pro Pro Asp Pro Val Gly Phe Ser Ala Arg Val	
485 490 495	
taattccggg gtttttaaaa gcgggttact tttgtttatg tattattccg tactagtttg	1722
aaaataatgg tattagagaa atg	1745

<210> 4

<211> 500  
 <212> PRT  
 <213> Dianthus caryophyllus

<400> 4

Met	His	Asn	Leu	Tyr	Tyr	Leu	Ile	Thr	Thr	Val	Phe	Arg	Gly	His	Gln
1				5					10					15	
Lys	Pro	Leu	Pro	Pro	Gly	Pro	Arg	Pro	Trp	Pro	Ile	Val	Gly	Asn	Leu
		20						25					30		
Pro	His	Met	Gly	Gln	Ala	Pro	His	Gln	Gly	Leu	Ala	Ala	Leu	Ala	Gln
		35					40					45			
Lys	Tyr	Gly	Pro	Leu	Leu	Tyr	Met	Arg	Leu	Gly	Tyr	Val	Asp	Val	Val
	50					55					60				
Val	Ala	Ala	Ser	Ala	Ser	Val	Ala	Thr	Gln	Phe	Leu	Lys	Thr	His	Asp
65					70					75					80
Leu	Asn	Phe	Ser	Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Ile	Ala
				85					90					95	
Tyr	Asn	Tyr	Gln	Asp	Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Lys	Trp	Arg
			100					105					110		
Met	Leu	Arg	Lys	Ile	Cys	Ser	Leu	His	Met	Phe	Ser	Ser	Lys	Ala	Leu
		115					120					125			
Asp	Asp	Phe	Arg	Leu	Val	Arg	Gln	Glu	Glu	Val	Ser	Ile	Leu	Val	Asn
	130					135					140				
Ala	Ile	Ala	Lys	Ala	Gly	Thr	Lys	Pro	Val	Gln	Leu	Gly	Gln	Leu	Leu
145					150					155					160
Asn	Val	Cys	Thr	Thr	Asn	Ala	Leu	Ser	Arg	Val	Met	Leu	Gly	Lys	Arg
				165					170					175	
Val	Leu	Gly	Asp	Gly	Thr	Gly	Lys	Ser	Asp	Pro	Lys	Ala	Glu	Glu	Phe
		180						185					190		
Lys	Asp	Met	Val	Leu	Glu	Leu	Met	Val	Leu	Thr	Gly	Val	Phe	Asn	Ile
		195					200					205			
Gly	Asp	Phe	Val	Pro	Ala	Leu	Glu	Cys	Leu	Asp	Leu	Gln	Gly	Val	Ala
	210					215					220				
Ser	Lys	Met	Lys	Lys	Leu	His	Lys	Arg	Leu	Asp	Asn	Phe	Met	Ser	Asn
225					230					235					240
Ile	Leu	Glu	Glu	His	Lys	Ser	Val	Ala	His	Gln	Gln	Asn	Gly	Gly	Asp
				245					250					255	
Leu	Leu	Ser	Ile	Leu	Ile	Ser	Leu	Lys	Asp	Asn	Cys	Asp	Gly	Glu	Gly
		260						265					270		
Gly	Lys	Phe	Ser	Ala	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asp	Leu	Phe
		275					280					285			
Thr	Ala	Gly	Thr	Asp	Thr	Ser	Ser	Ser	Thr	Thr	Glu	Trp	Ala	Ile	Ala
	290					295					300				
Glu	Leu	Ile	Arg	His	Pro	Lys	Ile	Leu	Ala	Gln	Val	Gln	Gln	Glu	Met
305					310					315					320
Asp	Ser	Val	Val	Gly	Arg	Asp	Arg	Leu	Ile	Ala	Glu	Ala	Asp	Ile	Pro
				325					330					335	
Asn	Leu	Thr	Tyr	Phe	Gln	Ala	Val	Ile	Lys	Glu	Val	Phe	Arg	Leu	His
		340						345					350		
Pro	Ser	Thr	Pro	Leu	Ser	Leu	Pro	Arg	Val	Ala	Asn	Glu	Ser	Cys	Glu
		355					360					365			
Ile	Asn	Gly	Tyr	His	Ile	Pro	Lys	Asn	Thr	Thr	Leu	Leu	Val	Asn	Val
	370					375					380				
Trp	Ala	Ile	Ala	Arg	Asp	Pro	Glu	Val	Trp	Ala	Asp	Pro	Leu	Glu	Phe
385					390					395					400
Lys	Pro	Glu	Arg	Phe	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Asn	Val	Asp	Val
				405					410					415	
Lys	Gly	Asn	Asp	Phe	Glu	Leu	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile





tac aac tat cag gac ttg gtc ttt gct cct tat ggc cca cgc tgg cgg	498
Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg	
125 130 135	
atg ctc agg aaa atc tgt gca ctc cac ctc ttc tcc gcc aaa gcc ttg	546
Met Leu Arg Lys Ile Cys Ala Leu His Leu Phe Ser Ala Lys Ala Leu	
140 145 150	
aac gac ttc aca cac gtc aga cag gat gag gtg ggg atc ctc act cgc	594
Asn Asp Phe Thr His Val Arg Gln Asp Glu Val Gly Ile Leu Thr Arg	
155 160 165	
gtt cta gca gat gca gga gaa acg ccg ttg aaa tta ggg cag atg atg	642
Val Leu Ala Asp Ala Gly Glu Thr Pro Leu Lys Leu Gly Gln Met Met	
170 175 180	
aac aca tgc gcc acc aat gca ata gcg cgt gtt atg ttg ggt cga cgc	690
Asn Thr Cys Ala Thr Asn Ala Ile Ala Arg Val Met Leu Gly Arg Arg	
185 190 195 200	
gtg gtt gga cac gca gac tca aag gcg gag gag ttt aag gca atg gta	738
Val Val Gly His Ala Asp Ser Lys Ala Glu Glu Phe Lys Ala Met Val	
205 210 215	
gtg gag ttg atg gta tta gct ggt gtg ttc aac tta ggt gat ttt atc	786
Val Glu Leu Met Val Leu Ala Gly Val Phe Asn Leu Gly Asp Phe Ile	
220 225 230	
cca cct ctt gaa aaa ttg gat ctt caa ggt gtc att gct aag atg aag	834
Pro Pro Leu Glu Lys Leu Asp Leu Gln Gly Val Ile Ala Lys Met Lys	
235 240 245	
aag ctt cac ttg cgt ttc gac tcg ttc ttg agt aag atc ctt gga gac	882
Lys Leu His Leu Arg Phe Asp Ser Phe Leu Ser Lys Ile Leu Gly Asp	
250 255 260	
cac aag atc aac agc tca gat gaa acc aaa ggc cat tcg gat ttg ttg	930
His Lys Ile Asn Ser Ser Asp Glu Thr Lys Gly His Ser Asp Leu Leu	
265 270 275 280	
aac atg tta att tct ttg aag gac gct gat gat gcc gaa gga ggg agg	978
Asn Met Leu Ile Ser Leu Lys Asp Ala Asp Asp Ala Glu Gly Gly Arg	
285 290 295	
ctc acc gac gta gaa att aaa gcg ttg ctc ttg aac ttg ttt gct gca	1026
Leu Thr Asp Val Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala	
300 305 310	
gga act gac aca aca tca agc act gtg gaa tgg tgc ata gct gag tta	1074
Gly Thr Asp Thr Thr Ser Ser Thr Val Glu Trp Cys Ile Ala Glu Leu	
315 320 325	
gta cga cat cct gaa atc ctt gcc caa gtc caa aaa gaa ctc gac tct	1122
Val Arg His Pro Glu Ile Leu Ala Gln Val Gln Lys Glu Leu Asp Ser	
330 335 340	
gtt gtt ggt aag aat cgg gtg gtg aag gag gct gat ctg gcc gga tta	1170

Val Val Gly Lys Asn Arg Val Val Lys Glu Ala Asp Leu Ala Gly Leu  
 345 350 355 360  
 cca ttc ctc caa gcg gtc gtc aag gaa aat ttc cga ctc cat ccc tcc 1218  
 Pro Phe Leu Gln Ala Val Val Lys Glu Asn Phe Arg Leu His Pro Ser  
 365 370 375  
 acc ccg ctc tcc cta ccg agg atc gca cat gag agt tgt gaa gtg aat 1266  
 Thr Pro Leu Ser Leu Pro Arg Ile Ala His Glu Ser Cys Glu Val Asn  
 380 385 390  
 gga tac ttg att cca aag ggt tcg aca ctt ctt gtc aat gtt tgg gca 1314  
 Gly Tyr Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala  
 395 400 405  
 att gct cgc gat cca aat gtg tgg gat gaa cca cta gag ttc cgg cct 1362  
 Ile Ala Arg Asp Pro Asn Val Trp Asp Glu Pro Leu Glu Phe Arg Pro  
 410 415 420  
 gaa cga ttc ttg aag ggc ggg gaa aag cct aat gtc gat gtt aga ggg 1410  
 Glu Arg Phe Leu Lys Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly  
 425 430 435 440  
 aat gat ttc gaa ttg ata ccg ttc gga gcg ggc cga aga att tgt gca 1458  
 Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala  
 445 450 455  
 gga atg agc tta gga ata cgt atg gtc cag ttg ttg aca gca act ttg 1506  
 Gly Met Ser Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Thr Leu  
 460 465 470  
 aac cat gcg ttt gac ttt gat ttg gcg gat gga cag ttg cct gaa agc 1554  
 Asn His Ala Phe Asp Phe Asp Leu Ala Asp Gly Gln Leu Pro Glu Ser  
 475 480 485  
 tta aac atg gag gaa gct tat ggg ctg acc ttg caa cga gct gac cct 1602  
 Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro  
 490 495 500  
 ttg gta gtg cac ccg aag cct agg tag gcacctcatg tttatcaaac 1649  
 Leu Val Val His Pro Lys Pro Arg  
 505 510  
 ttaggactca tggttagaga acctcttggt gttttatcag attgaagtgt gatgtccaag 1709  
 ac 1711

<210> 6  
 <211> 512  
 <212> PRT  
 <213> Antirrhinum majus

<400> 6  
 Met Gln His Gln Tyr Tyr Ser Leu Ile Thr Met Asp Asp Ile Ser Ile  
 1 5 10 15  
 Thr Ser Leu Leu Val Pro Cys Thr Phe Ile Leu Gly Phe Leu Leu Leu

				20						25					30		
Tyr	Ser	Phe	Leu	Asn	Lys	Lys	Val	Lys	Pro	Leu	Pro	Pro	Gly	Pro	Lys		
		35					40					45					
Pro	Trp	Pro	Ile	Val	Gly	Asn	Leu	Pro	His	Leu	Gly	Pro	Lys	Pro	His		
	50					55					60						
Gln	Ser	Met	Ala	Ala	Leu	Ala	Arg	Val	His	Gly	Pro	Leu	Ile	His	Leu		
65					70					75					80		
Lys	Met	Gly	Phe	Val	His	Val	Val	Val	Ala	Ser	Ser	Ala	Ser	Val	Ala		
				85					90					95			
Glu	Lys	Phe	Leu	Lys	Val	His	Asp	Ala	Asn	Phe	Ser	Ser	Arg	Pro	Pro		
			100					105					110				
Asn	Ser	Gly	Ala	Lys	His	Val	Ala	Tyr	Asn	Tyr	Gln	Asp	Leu	Val	Phe		
		115					120					125					
Ala	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Leu	Arg	Lys	Ile	Cys	Ala	Leu		
		130				135					140						
His	Leu	Phe	Ser	Ala	Lys	Ala	Leu	Asn	Asp	Phe	Thr	His	Val	Arg	Gln		
145					150					155					160		
Asp	Glu	Val	Gly	Ile	Leu	Thr	Arg	Val	Leu	Ala	Asp	Ala	Gly	Glu	Thr		
				165					170					175			
Pro	Leu	Lys	Leu	Gly	Gln	Met	Met	Asn	Thr	Cys	Ala	Thr	Asn	Ala	Ile		
			180					185					190				
Ala	Arg	Val	Met	Leu	Gly	Arg	Arg	Val	Val	Gly	His	Ala	Asp	Ser	Lys		
		195					200					205					
Ala	Glu	Glu	Phe	Lys	Ala	Met	Val	Val	Glu	Leu	Met	Val	Leu	Ala	Gly		
		210				215					220						
Val	Phe	Asn	Leu	Gly	Asp	Phe	Ile	Pro	Pro	Leu	Glu	Lys	Leu	Asp	Leu		
225					230					235					240		
Gln	Gly	Val	Ile	Ala	Lys	Met	Lys	Lys	Leu	His	Leu	Arg	Phe	Asp	Ser		
				245					250					255			
Phe	Leu	Ser	Lys	Ile	Leu	Gly	Asp	His	Lys	Ile	Asn	Ser	Ser	Asp	Glu		
			260					265					270				
Thr	Lys	Gly	His	Ser	Asp	Leu	Leu	Asn	Met	Leu	Ile	Ser	Leu	Lys	Asp		
		275					280					285					
Ala	Asp	Asp	Ala	Glu	Gly	Gly	Arg	Leu	Thr	Asp	Val	Glu	Ile	Lys	Ala		
		290				295				300							
Leu	Leu	Leu	Asn	Leu	Phe	Ala	Ala	Gly	Thr	Asp	Thr	Thr	Ser	Ser	Thr		
305					310					315					320		
Val	Glu	Trp	Cys	Ile	Ala	Glu	Leu	Val	Arg	His	Pro	Glu	Ile	Leu	Ala		
			325						330					335			
Gln	Val	Gln	Lys	Glu	Leu	Asp	Ser	Val	Val	Gly	Lys	Asn	Arg	Val	Val		
			340					345					350				

485                      490                      495  
 Leu Thr Leu Gln Arg Ala Asp Pro Leu Val Val His Pro Lys Pro Arg  
 500                      505                      510

<210> 7  
 <211> 971  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(813)

<400> 7  
 gat atg ctt agc act tta atc tcc ctt aaa gga act gat ctt gac ggt 48  
 Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly  
 1                      5                      10                      15  
  
 gac gga gga agc tta acg gat act gag att aaa gcc ttg cta ttg aac 96  
 Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn  
 20                      25                      30  
  
 atg ttc aca gct gga act gac acg tca gca agt acg gtg gac tgg gct 144  
 Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala  
 35                      40                      45  
  
 ata gct gaa ctt atc cgt cac ccg gat ata atg gtt aaa gcc caa gaa 192  
 Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu  
 50                      55                      60  
  
 gaa ctt gat att gtt gtg ggc cgt gac agg cct gtt aat gaa tca gac 240  
 Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp  
 65                      70                      75                      80  
  
 atc gct cag ctt cct tac ctt cag gcg gtt atc aaa gag aat ttc agg 288  
 Ile Ala Gln Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Asn Phe Arg  
 85                      90                      95  
  
 ctt cat cca cca aca cca ctc tcg tta cca cac atc gcg tca gag agc 336  
 Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser  
 100                      105                      110  
  
 tgt gag atc aac ggc tac cat atc ccg aaa gga tcg act cta ttt gac 384  
 Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp  
 115                      120                      125  
  
 gga cat atg ggc cta ggc cgt gac ccg gat caa tgg tcc gac ccg tta 432  
 Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu  
 130                      135                      140  
  
 gca ttt aaa ccc gag aga ttc tta ccc ggt ggt gaa aaa tcc ggc gtt 480  
 Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Ser Gly Val  
 145                      150                      155                      160  
  
 gat gtg aaa gga agc gat ttc gag cta ata ccg ttc ggg gct ggg agg 528  
 Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg

165										170					175					
cca atc tgt gca ggt tta agt tta ggg cta cgt aca gat tta agt tgc	576																			
Pro Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Asp Leu Ser Cys																				
180 185 190																				
ctt cac gcc aac gtt gct cac aag cat ttg att ggg aac ttc agc tgg	624																			
Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp																				
195 200 205																				
aga agt tac gcc gga caa cct gaa tat cgc agg aaa agt tta ctg ggc	672																			
Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly																				
210 215 220																				
ttt aca ctg caa aga gcg gtt cct tcg gtg gta cac cct aag cca agg	720																			
Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg																				
225 230 235 240																				
ttg gcc ccg aac gtt tat gga ccc cgg gtc ggc tta aaa ttt aac ttt	768																			
Leu Ala Pro Asn Val Tyr Gly Pro Arg Val Gly Leu Lys Phe Asn Phe																				
245 250 255																				
gct tct tgg aca agg tat atg gct tgc acg aaa cta acg ttt taa	813																			
Ala Ser Trp Thr Arg Tyr Met Ala Cys Thr Lys Leu Thr Phe																				
260 265 270																				
cacaccgtag tttgatccgg agttagcttt atgtaagaac gtgtaacgcc aaatcaagcc	873																			
attatcaact accgtgagct gtttgtaccc tatctataaa tcttgaagag gaacatttca	933																			
gaactcttga ctatgtttca ggaacaaaaa aaaaaaaa	971																			

<210> 8  
 <211> 270  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 8  
 Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly  
 1 5 10 15  
 Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn  
 20 25 30  
 Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala  
 35 40 45  
 Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu  
 50 55 60  
 Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp  
 65 70 75 80  
 Ile Ala Gln Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Asn Phe Arg  
 85 90 95  
 Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser  
 100 105 110  
 Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp  
 115 120 125  
 Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu  
 130 135 140

Ala	Phe	Lys	Pro	Glu	Arg	Phe	Leu	Pro	Gly	Gly	Glu	Lys	Ser	Gly	Val
145					150					155					160
Asp	Val	Lys	Gly	Ser	Asp	Phe	Glu	Leu	Ile	Pro	Phe	Gly	Ala	Gly	Arg
			165						170					175	
Pro	Ile	Cys	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Arg	Thr	Asp	Leu	Ser	Cys
			180					185					190		
Leu	His	Ala	Asn	Val	Ala	His	Lys	His	Leu	Ile	Gly	Asn	Phe	Ser	Trp
	195						200					205			
Arg	Ser	Tyr	Ala	Gly	Gln	Pro	Glu	Tyr	Arg	Arg	Lys	Ser	Leu	Leu	Gly
	210				215						220				
Phe	Thr	Leu	Gln	Arg	Ala	Val	Pro	Ser	Val	Val	His	Pro	Lys	Pro	Arg
225				230					235						240
Leu	Ala	Pro	Asn	Val	Tyr	Gly	Pro	Arg	Val	Gly	Leu	Lys	Phe	Asn	Phe
			245					250						255	
Ala	Ser	Trp	Thr	Arg	Tyr	Met	Ala	Cys	Thr	Lys	Leu	Thr	Phe		
			260					265					270		

<210> 9  
 <211> 6595  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1478)..(1927)

<220>  
 <221> CDS  
 <222> (2651)..(3091)

<220>  
 <221> CDS  
 <222> (3170)..(3340)

<220>  
 <221> CDS  
 <222> (3421)..(3897)

<400> 9	
gtcgactctc tccctttcgc ttgctacttt ttctacataa ataaatgcaa tgataaattt	60
gtgcacacat tcgtatgttt gaaacatggg aggatccaca atttatactt tatagactca	120
aaatggaaaa gaaacgtaca ttataaattt atctgcaatt tgttttctct tgctaaacta	180
gactgtataa taacctctgt atatgctatt actcgattgt aaacgtaccc cgcaagtcgc	240
aagcaaggta aataaagtat aatttatatt tcacacacga aactttaatt attattttta	300
tcacttgcag attaacagta aaaaaaaaaa aaatgtgact ttaacggcga caaaaaactac	360
tgatctttct ccaatattta aataatataa ttaataaacg tcttttcata cttgtatttt	420
ccgacccgag ttctgaaagt gaaaacatat ggtactagat attctcgatt tgtttttag	480
ccactagact ctaaacagaa aaaagaagcc aaaaggacaa cgtaaataaaa gagacactgt	540

tattaaaagt tagaaaccaa acggtgaaaa tccagctaca tacataaaat aaagccaagg	600
taccaaacta atgaactgta acctcttttt tcttttcttt tttgttaaag gatttatgaa	660
ctgtaactta gaatgcttgg tttgtgggca gtgtaataata tgacacacat gcattttttt	720
tgtttgtaa ataggaagac ttcttttttc tttatcaact tccttatttt cataaaacaa	780
aacactgaaa aaagtacaga tgttctcacg tacgtcacgt gtacatacat atatattaga	840
ccactatata ataagatatg aagtgttagg tttaaatcaa ttaacgaatc ccatccaaat	900
gatgaaacag ttaacaagaa atcaaaatag tttattaggg ttacaatgat tttatacttt	960
taagaaatct tagaacctat cacttacaaa tgagtaaag accattactc ctcgagaatc	1020
taaggcgctt aaggaagcat tgcgaatcgg gtgtgaaaaa gatctatttt ttgaattatt	1080
tcacacaatt tcttaatgtc aattttcgat gctcccatat tctccacggg ttaaagcaag	1140
attggtggga aagggatatt ctgcacatga ttacaatgaa atatgggttg aaaaaaaaaa	1200
aaaaaaaaatta ctcaatgttg caccaaaaac cagaaaactc taagttgcgc taataaaaaa	1260
aaaagttata aaccaacat caaaccaaaa ccgtactaaa ctgtcccata tgagatttag	1320
ctttaaataa attagtactt ctcataacga taactaaatt aaatttcctt agccaagaca	1380
tacatatagt tttgattgac aaaaaaaaaa aaaactcctc tatttatagc ttgtgttttg	1440
tttctcatt tttcacttac cattcaaacc caacact atg gca act cta ttt ctc	1495
Met Ala Thr Leu Phe Leu	
1 5	
aca atc ctc cta gcc act gtc ctc ttc ctc atc ctc cgt atc ttc tct	1543
Thr Ile Leu Leu Ala Thr Val Leu Phe Leu Ile Leu Arg Ile Phe Ser	
10 15 20	
cac cgt cgc aac cgc agc cac aac aac cgt ctt cca ccg ggg cca aac	1591
His Arg Arg Asn Arg Ser His Asn Asn Arg Leu Pro Pro Gly Pro Asn	
25 30 35	
cca tgg ccc atc atc gga aac ctc cct cac atg ggc act aag cct cat	1639
Pro Trp Pro Ile Ile Gly Asn Leu Pro His Met Gly Thr Lys Pro His	
40 45 50	
cga acc ctt tcc gcc atg gtt act act tac ggc cct atc ctc cac ctc	1687
Arg Thr Leu Ser Ala Met Val Thr Thr Tyr Gly Pro Ile Leu His Leu	
55 60 65 70	
cga cta ggg ttc gta gac gtc gtg gtc gcc gct tct aaa tcc gtg gcc	1735
Arg Leu Gly Phe Val Asp Val Val Val Ala Ala Ser Lys Ser Val Ala	
75 80 85	
gag cag ttc ttg aaa ata cac gac gcc aat ttc gct agc cga cca cca	1783
Glu Gln Phe Leu Lys Ile His Asp Ala Asn Phe Ala Ser Arg Pro Pro	
90 95 100	



aac tca gga gcc aaa cac atg gca tat aac tat caa gat ctt gtc ttt	1831
Asn Ser Gly Ala Lys His Met Ala Tyr Asn Tyr Gln Asp Leu Val Phe	
105 110 115	
gca cct tac gga cac cga tgg aga ctg ttg aga aag att agt tct gtt	1879
Ala Pro Tyr Gly His Arg Trp Arg Leu Leu Arg Lys Ile Ser Ser Val	
120 125 130	
cat cta ttt tca gct aaa gct ctc gaa gat ttc aaa cat gtt cga cag	1927
His Leu Phe Ser Ala Lys Ala Leu Glu Asp Phe Lys His Val Arg Gln	
135 140 145 150	
gtaaaacaat tataaacggt attctcattt tctaacgcta tagctcactg gacctgaatc	1987
atgtcatttc aatgttttga ctttttcttt atatatacat aattataatt tataattggg	2047
atttcaaacc ctatctctca ctatttcaag actagaccgg attggaattt gaacttttgt	2107
aatgaatatt agtatctgca cataaatttt atgttaaagt tgggttttct taaagtgaat	2167
ttatatatta aaaatatata aacgattggg ttttactcaa atgaatttac ataagagcta	2227
gggtataagtg caaatatgca atactgtcat tgtcgtggat gtataaaaagt atgatctaac	2287
tttgatgatg ccatggaaaa attggaaagt tcagatccag aggaaacatt gcttgaatta	2347
taaaatgtat ggaccacatt gtttccttaa atggaaggtc tcacgagttt ctcaatttca	2407
gactactgat aatatatgct attatagatt ttattttctg attatttttt ttggtttaat	2467
ttaattagag taaattttta aaaagaaata tatggttttg ttaaccgtgt tttaaaattt	2527
gatagagctt ttagatcata atcataattt tttcgtatta attgtgatta tgttggacga	2587
aaataacttaa ttagtattca agaaaactct tattctaaaa acagaaataa atgaatttta	2647
cag gaa gag gtt gga acg cta acg cgg gag cta gtg cgt gtt ggc acg	2695
Glu Glu Val Gly Thr Leu Thr Arg Glu Leu Val Arg Val Gly Thr	
1 5 10 15	
aaa ccc gtg aat tta ggc cag ttg gtg aac atg tgt gta gtc aac gct	2743
Lys Pro Val Asn Leu Gly Gln Leu Val Asn Met Cys Val Val Asn Ala	
20 25 30	
cta gga cga gag atg atc gga cgg cga ctg ttc ggc gcc gac gcc gat	2791
Leu Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp	
35 40 45	
cat aaa gct gac gag ttt cga tcg atg gtg acg gaa atg atg gct ctc	2839
His Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu	
50 55 60	
gcc gga gta ttt aac atc gga gat ttc gtg ccg tca ctt gat tgg tta	2887
Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu	
65 70 75	
gat tta caa ggc gtc gct ggt aaa atg aaa cgg ctt cac aaa aga ttc	2935

Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe	
80 85 90 95	
gac gct ttt cta tcg tcg att ttg aaa gag cac gaa atg aac ggt caa	2983
Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln	
100 105 110	
gat caa aag cat aca gat atg ctt agc act tta atc tcc ctt aaa gga	3031
Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly	
115 120 125	
act gat ctt gac ggt gac gga gga agc tta acg gat act gag att aaa	3079
Thr Asp Leu Asp Gly Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys	
130 135 140	
gcc ttg cta ttg gtcagttttt tgacaattaa tttccttaaa aatcgtatat	3131
Ala Leu Leu Leu	
145	
aatgaaagtt agattgtttt ttttggttgt aaatacag aac atg ttc aca gct	3184
Asn Met Phe Thr Ala	
1 5	
gga act gac acg tca gca agt acg gtg gac tgg gct ata gct gaa ctt	3232
Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala Ile Ala Glu Leu	
10 15 20	
atc cgt cac ccg gat ata atg gtt aaa gcc caa gaa gaa ctt gat att	3280
Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu Glu Leu Asp Ile	
25 30 35	
gtt gtg ggc cgt gac agg cct gtt aat gaa tca gac atc gct cag ctt	3328
Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp Ile Ala Gln Leu	
40 45 50	
cct tac ctt cag gtaccgttaa cccaaaccgg aatttgaat tgttttggtt	3380
Pro Tyr Leu Gln	
55	
agcgagctat tgttgttaat ccggttttgg tttaaaacag gcg gtt atc aaa gag	3435
Ala Val Ile Lys Glu	
1 5	
aat ttc agg ctt cat cca cca aca cca ctc tcg tta cca cac atc gcg	3483
Asn Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala	
10 15 20	
tca gag agc tgt gag atc aac ggc tac cat atc ccg aaa gga tcg act	3531
Ser Glu Ser Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr	
25 30 35	
cta ttg acg aac ata tgg gcc ata gcc cgt gac ccg gat caa tgg tcc	3579
Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp Pro Asp Gln Trp Ser	
40 45 50	
gac ccg tta gca ttt aaa ccc gag aga ttc tta ccc ggt ggt gaa aaa	3627
Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys	
55 60 65	

tcc ggc gtt gat gtg aaa gga agc gat ttc gag cta ata ccg ttc gga	3675
Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly	
70 75 80 85	
gct ggg agg aga atc tgt gcc ggt tta agt tta ggg tta cgt acg att	3723
Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Ile	
90 95 100	
cag ttt ctt acg gcg acg ttg gtt caa gga ttt gat tgg gaa tta gct	3771
Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe Asp Trp Glu Leu Ala	
105 110 115	
gga gga gtt acg ccg gag aag ctg aat atg gag gag agt tat ggg ctt	3819
Gly Gly Val Thr Pro Glu Lys Leu Asn Met Glu Glu Ser Tyr Gly Leu	
120 125 130	
aca ctg caa aga gcg gtt cct ttg gtg gta cat cct aag cca agg ttg	3867
Thr Leu Gln Arg Ala Val Pro Leu Val Val His Pro Lys Pro Arg Leu	
135 140 145	
gct ccg aac gtt tat gga ctc ggg tcg ggt taaaatttaa ctttgcttct	3917
Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly	
150 155	
tggaacaagg atattggcttg cacgaaaata aagtttttaa acagcgtagt ttgatccgga	3977
gttagcttta tgtaagaacg tgtaacgcca aatcaagtca ttattaaata ttgtgagttg	4037
tttgtaacct atatataaat cttgaagagg aagatttcag aaatcttgaa tatgttttag	4097
gaaaaacatt gtttttttta cagtagcgca agttgaatta aaacctattc cttacagaac	4157
caaatgcatt aataattcta gatatttttg gccaaagacaa tcagattttt caatatttca	4217
tatatactag gtggaacacc accacctgca actctgcaac acatgttacg ttacacaatc	4277
acttttggcg gttttcaatt atttatataa aattgtaaat gtttgtagac agtagaaaat	4337
tagtaatagt gaattttgtt tctccgaata tgtatagcaa tatatatggc atggatcaaa	4397
ctagccgaca tcctaacttg ttcacagctt tcctttttac ttatctagtc gattaagcat	4457
cagaaagtat gttttaattt ttaaatttga aaaagggtgta cttacaagtt cgggtgttca	4517
cacggaggag agctacaata atgaaaaagc tgactcaaga agggctatag aagaaacaag	4577
agtcacggaa caagttgtca ctctcaatct ccagtacact agcttccata actctctctc	4637
tttctctctt tcttctctct ctaaaagtta tcagaataga aatctctctc tctcaacaag	4697
tctaacagtg ccatttgat ctctgaactc caacatggct cctctgggtc tctaccttct	4757
cactctctct atggctggcc attccagtaa gaactctcac tgatcttctt cacctttgtt	4817
tatggatttg gtctctcagt ctactctcg cttacccttt cacattcagc tctggctctc	4877
tggtttaaga aacccttaat ctacaaagct tgctttctct gcaaatgaac taccttactt	4937
atctcttatg caactcttgt tgatgatttg caaacatott aacctctcga aacaagattt	4997

acaaatctta ctggcttcac ttacaatttt gttccattt ttttcttctt tggtaggtgc	5057
ctcatggtgt gtgtgcaaaa cagggtgag tgactcagt ctacaaaaga cattagacta	5117
tgcttggtga aatggagctg actgtaaccc aactcaccca aaaggctctt gttcaatcc	5177
tgacaatggt agggctcatt gcaactatgc agtcaatagc ttcttccaaa agaaagggtca	5237
agcttctgag tcttgtaact tcaactggtac tgccactctt accaccaccg atcccagtaa	5297
gttttcagaa tgttaacact cttgtgatct ttagaaccct aaaaaatttt gagtctcaga	5357
aagttcaagt tcaaggctctt ttgggttagag tactaaagat tcaagtagag actaggcggtg	5417
agatattttt tctctgatgt gtgatttttt ggcacaggct atacaggatg tgcattccct	5477
tctagtgcta ggtacggctc tttgcttctc tacacattta ttttcttaat ggctttatct	5537
agaactttga aggataccat tttatttttt ttggacaaag aaggatagcc atttaatact	5597
acactttaat gttggattaa ctaacttatt atgcctattt aatggcctac actttaagtg	5657
gacacaagct tgatttggtt ataaaaaaag tgcactataa tcttatttta ctgaaccctt	5717
ttttctatga tttttttact aaactttaga taacatctac aacaattcaa ttgccttttt	5777
ttggggattg tataagtttg aacctatggt tagtgtattg acttgcgctt ctcttattgc	5837
aacggttctt tgaaaacaca ttaatgataa ataaattgaa aagtatagag atggcaattg	5897
tttcaaaagc taatctttct gcttgctaact actttacata aaaaacaaaa aattaagaag	5957
attttcaaac aatacaactt ttttaccttg tcttaacaaa ttcaactcaa atgacatgtg	6017
tttgctttta aatagtaaca actgtaaatt catttgctct tgagacataa gtgcaagcta	6077
aagataaacg caagcaatac aattaggctt aattaagatt acgaatattg ttgtttgttt	6137
atagtggttc tagtggaagc ggtagcacca ccgtgacgcc aggcaaaaac agtccaaaag	6197
gaagcaacag catcaccaca tttcccggcg gaaacagtcc atacactggc acaccatcca	6257
ccggtattat aggaggcaat atcactgatg caactggaac cgggttgaac ccggtattact	6317
caaccgaaag cagtggattt gcgctctatt actccaacaa cttctgttta accggctttt	6377
gttctctcgt gatgatgctc tgaagaagaa tcaccgtctt cttttagttt atgetttagtc	6437
aaaaaaatat gttatttata tgttcttggt gttttagaga taatttaatc tggatttcgg	6497
ttctttttta ctttccggtt ttaagaaaac aattatcaat gtaaaaacaa atctactatc	6557
gatcggtttg gtacgaattc ctgcagcccg ggggatcc	6595

<210> 10  
 <211> 150  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 10  
Met Ala Thr Leu Phe Leu Thr Ile Leu Leu Ala Thr Val Leu Phe Leu  
1 5 10 15  
Ile Leu Arg Ile Phe Ser His Arg Arg Asn Arg Ser His Asn Asn Arg  
20 25 30  
Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His  
35 40 45  
Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr  
50 55 60  
Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala  
65 70 75 80  
Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn  
85 90 95  
Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn  
100 105 110  
Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu  
115 120 125  
Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp  
130 135 140  
Phe Lys His Val Arg Gln  
145 150

<210> 11  
<211> 147  
<212> PRT  
<213> Arabidopsis thaliana

<400> 11  
Glu Glu Val Gly Thr Leu Thr Arg Glu Leu Val Arg Val Gly Thr Lys  
1 5 10 15  
Pro Val Asn Leu Gly Gln Leu Val Asn Met Cys Val Val Asn Ala Leu  
20 25 30  
Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp His  
35 40 45  
Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu Ala  
50 55 60  
Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu Asp  
65 70 75 80  
Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe Asp  
85 90 95  
Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln Asp

100                      105                      110  
 Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr  
           115                      120                      125  
 Asp Leu Asp Gly Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala  
           130                      135                      140  
 Leu Leu Leu  
 145

<210> 12  
 <211> 57  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 12  
 Asn Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp  
           1                      5                      10                      15  
 Ala Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln  
                   20                      25                      30  
 Glu Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser  
           35                      40                      45  
 Asp Ile Ala Gln Leu Pro Tyr Leu Gln  
           50                      55

<210> 13  
 <211> 159  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 13  
 Ala Val Ile Lys Glu Asn Phe Arg Leu His Pro Pro Thr Pro Leu Ser  
           1                      5                      10                      15  
 Leu Pro His Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr His Ile  
                   20                      25                      30  
 Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp  
           35                      40                      45  
 Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu  
           50                      55                      60  
 Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu  
           65                      70                      75                      80  
 Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu  
                   85                      90                      95

Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe  
100 105 110

Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn Met Glu  
115 120 125

Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val Val His  
130 135 140

Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly  
145 150 155

<210> 14  
<211> 1748  
<212> DNA  
<213> Rosa hybrida

<220>  
<221> CDS  
<222> (22)..(1563)

<400> 14  
tgtcgaagaaa gaagaacagc c atg ttt ctc ata gta gtg atc acc ttc ctc 51  
Met Phe Leu Ile Val Val Ile Thr Phe Leu 10  
1

ttc gcc gtg ttt ttg ttc cgg ctt ctt ttc tcc ggc aaa tcc caa cgc 99  
Phe Ala Val Phe Leu Phe Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg 25  
15 20

cac tcg ctc cct ctc cct cct ggc ccc aaa cca tgg ccg gtg gtt ggc 147  
His Ser Leu Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Val Val Gly 40  
30 35

aac tta cct cac ttg ggc ccc ttc ccg cac cac tcc atc gcg gag ttg 195  
Asn Leu Pro His Leu Gly Pro Phe Pro His His Ser Ile Ala Glu Leu 55  
45 50

gcg aag aaa cac ggg ccg ctc atg cac ctc cgc ctc ggc tac gtt gac 243  
Ala Lys Lys His Gly Pro Leu Met His Leu Arg Leu Gly Tyr Val Asp 70  
60 65

gta gtc gtg gcg gca tca gca tcc gta gcg gcc cag ttc ttg aag act 291  
Val Val Val Ala Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr 90  
75 80 85

cac gac gcc aat ttc tcc agc cga ccg ccc aac tcc ggc gcc aag cac 339  
His Asp Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His 105  
95 100

ctc gcc tat aac tac cag gac ctc gtg ttc agg ccg tac ggt cca cgg 387  
Leu Ala Tyr Asn Tyr Gln Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg 120  
110 115

tgg cgc atg ttc ccg aag atc agc tcc gtc cat ctg ttc tcc ggc aaa 435  
Trp Arg Met Phe Arg Lys Ile Ser Ser Val His Leu Phe Ser Gly Lys 135  
125 130

gcc ttg gat gat ctt aaa cac gtc cgg cag gag gag gta agt gtg cta	483
Ala Leu Asp Asp Leu Lys His Val Arg Gln Glu Glu Val Ser Val Leu	
140 145 150	
gcg cat gcc ttg gca aat tca ggg tca aag gta gtg aac ctg gcg caa	531
Ala His Ala Leu Ala Asn Ser Gly Ser Lys Val Val Asn Leu Ala Gln	
155 160 165 170	
ctg ctg aac ctg tgc acg gtc aat gct cta gga agg gtg atg gta ggg	579
Leu Leu Asn Leu Cys Thr Val Asn Ala Leu Gly Arg Val Met Val Gly	
175 180 185	
cgg agg gtt ttc ggc gac ggc agc gga ggc gac gat ccg aag gcg gac	627
Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp	
190 195 200	
gag ttc aaa tcg atg gtg gtg gag atg atg gtg ttg gca gga gtg ttc	675
Glu Phe Lys Ser Met Val Val Glu Met Met Val Leu Ala Gly Val Phe	
205 210 215	
aac ata ggt gac ttc atc ccc tct ctc gaa tgg ctt gac ttg caa ggc	723
Asn Ile Gly Asp Phe Ile Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly	
220 225 230	
gtg gcg tcc aag atg aag aag ctc cac aag aga ttc gac gac ttc ttg	771
Val Ala Ser Lys Met Lys Lys Leu His Lys Arg Phe Asp Asp Phe Leu	
235 240 245 250	
aca gcc att gtc gag gac cac aag aag ggc tcc ggc acg gcg ggg cac	819
Thr Ala Ile Val Glu Asp His Lys Lys Gly Ser Gly Thr Ala Gly His	
255 260 265	
gtc gac atg ttg acc act ctg ctc tcg ctc aag gaa gac gcc gac ggc	867
Val Asp Met Leu Thr Thr Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly	
270 275 280	
gaa gga ggc aag ctc acc gat act gaa atc aaa gct ttg ctt ttg aac	915
Glu Gly Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn	
285 290 295	
atg ttc acg gct ggc act gat acg tca tcg agc acg gtg gaa tgg gca	963
Met Phe Thr Ala Gly Thr Asp Thr Ser Ser Thr Thr Val Glu Trp Ala	
300 305 310	
ata gct gaa ctc att cgg cac cct cat atg cta gcg cga gtt cag aaa	1011
Ile Ala Glu Leu Ile Arg His Pro His Met Leu Ala Arg Val Gln Lys	
315 320 325 330	
gag ctt gac gat ttt gtt ggc cat gac cga ctt gtg acc gaa tcc gac	1059
Glu Leu Asp Asp Phe Val Gly His Asp Arg Leu Val Thr Glu Ser Asp	
335 340 345	
ata ccc aac ctc cct tac ctc caa gcc gtg atc aag gaa acg ttc cga	1107
Ile Pro Asn Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Phe Arg	
350 355 360	
ctc cac cca tcc act cct ctc tcg ttg cct cgt atg gca gcc gag agt	1155
Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ala Glu Ser	
365 370 375	



tgc gaa atc aac ggg tac cac atc ccg aaa ggc tcc aca ctc ttg gtc 1203  
 Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Leu Val  
 380 385 390

aat gta tgg gcc ata tcg cgt gac ccg gct gaa tgg gcc gac cca ctg 1251  
 Asn Val Trp Ala Ile Ser Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu  
 395 400 405 410

gag ttc aag ccc gag agg ttc ctg ccg ggg ggc gaa aag cct aat gtt 1299  
 Glu Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val  
 415 420 425

gat att aga gga aac gat ttt gaa gtc ata ccc ttc ggt gcc ggg cga 1347  
 Asp Ile Arg Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg  
 430 435 440

aga ata tgt gcc ggg atg agc ttg ggc ctg cgt atg gtc cat tta atg 1395  
 Arg Ile Cys Ala Gly Met Ser Leu Gly Leu Arg Met Val His Leu Met  
 445 450 455

act gca aca ttg gtc cac gca ttt aat tgg gcc ttg gct gat ggg ctg 1443  
 Thr Ala Thr Leu Val His Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu  
 460 465 470

acc gct gag aag tta aac atg gat gaa gca tat ggg ctc act cta caa 1491  
 Thr Ala Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln  
 475 480 485 490

cga gct gca ccg tta atg gtg cac ccg cgc acc agg ctg gcc cca cag 1539  
 Arg Ala Ala Pro Leu Met Val His Pro Arg Thr Arg Leu Ala Pro Gln  
 495 500 505

gca tat aaa act tca tca tct taa ttagagagct atgttctggg tgtgcccggt 1593  
 Ala Tyr Lys Thr Ser Ser Ser  
 510

ttgatgtctc catgttttct atttaggttt aaatctgtaa gataagggtga ttctatgctg 1653

aatcacaaaa gttgctatct aaattccatg tccaatgaaa acgttcttct tcccttctta 1713

taatttatga atacttatga tataggcgac agcaa 1748

<210> 15

<211> 513

<212> PRT

<213> Rosa hybrida

<400> 15

Met Phe Leu Ile Val Val Ile Thr Phe Leu Phe Ala Val Phe Leu Phe  
 1 5 10 15  
 Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg His Ser Leu Pro Leu Pro  
 20 25 30  
 Pro Gly Pro Lys Pro Trp Pro Val Val Gly Asn Leu Pro His Leu Gly  
 35 40 45  
 Pro Phe Pro His His Ser Ile Ala Glu Leu Ala Lys Lys His Gly Pro  
 50 55 60  
 Leu Met His Leu Arg Leu Gly Tyr Val Asp Val Val Val Ala Ala Ser

65					70					75					80
Ala	Ser	Val	Ala	Ala	Gln	Phe	Leu	Lys	Thr	His	Asp	Ala	Asn	Phe	Ser
				85					90					95	
Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Leu	Ala	Tyr	Asn	Tyr	Gln
			100					105					110		
Asp	Leu	Val	Phe	Arg	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Phe	Arg	Lys
		115					120					125			
Ile	Ser	Ser	Val	His	Leu	Phe	Ser	Gly	Lys	Ala	Leu	Asp	Asp	Leu	Lys
	130					135					140				
His	Val	Arg	Gln	Glu	Glu	Val	Ser	Val	Leu	Ala	His	Ala	Leu	Ala	Asn
145					150					155					160
Ser	Gly	Ser	Lys	Val	Asn	Leu	Ala	Gln	Leu	Leu	Asn	Leu	Cys	Thr	
			165					170					175		
Val	Asn	Ala	Leu	Gly	Arg	Val	Met	Val	Gly	Arg	Arg	Val	Phe	Gly	Asp
		180					185						190		
Gly	Ser	Gly	Gly	Asp	Asp	Pro	Lys	Ala	Asp	Glu	Phe	Lys	Ser	Met	Val
	195					200						205			
Val	Glu	Met	Met	Val	Leu	Ala	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile
	210					215					220				
Pro	Ser	Leu	Glu	Trp	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	Met	Lys
225					230					235					240
Lys	Leu	His	Lys	Arg	Phe	Asp	Asp	Phe	Leu	Thr	Ala	Ile	Val	Glu	Asp
			245					250						255	
His	Lys	Lys	Gly	Ser	Gly	Thr	Ala	Gly	His	Val	Asp	Met	Leu	Thr	Thr
		260				265						270			
Leu	Leu	Ser	Leu	Lys	Glu	Asp	Ala	Asp	Gly	Glu	Gly	Gly	Lys	Leu	Thr
	275					280					285				
Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Met	Phe	Thr	Ala	Gly	Thr
	290				295					300					
Asp	Thr	Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg
305					310					315					320
His	Pro	His	Met	Leu	Ala	Arg	Val	Gln	Lys	Glu	Leu	Asp	Asp	Phe	Val
			325					330						335	
Gly	His	Asp	Arg	Leu	Val	Thr	Glu	Ser	Asp	Ile	Pro	Asn	Leu	Pro	Tyr
		340					345					350			
Leu	Gln	Ala	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro
	355					360					365				
Leu	Ser	Leu	Pro	Arg	Met	Ala	Ala	Glu	Ser	Cys	Glu	Ile	Asn	Gly	Tyr
	370				375					380					
His	Ile	Pro	Lys	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ser
385					390					395					400
Arg	Asp	Pro	Ala	Glu	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Lys	Pro	Glu	Arg
			405					410					415		
Phe	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Asn	Val	Asp	Ile	Arg	Gly	Asn	Asp
		420					425					430			
Phe	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met
	435					440					445				
Ser	Leu	Gly	Leu	Arg	Met	Val	His	Leu	Met	Thr	Ala	Thr	Leu	Val	His
	450				455					460					
Ala	Phe	Asn	Trp	Ala	Leu	Ala	Asp	Gly	Leu	Thr	Ala	Glu	Lys	Leu	Asn
465					470					475					480
Met	Asp	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Ala	Pro	Leu	Met
			485					490					495		
Val	His	Pro	Arg	Thr	Arg	Leu	Ala	Pro	Gln	Ala	Tyr	Lys	Thr	Ser	Ser
		500					505						510		

Ser

<211> 1660  
 <212> DNA  
 <213> Chrysanthemum

<220>  
 <221> CDS  
 <222> (4)..(1530)

<400> 16

aaa atg acc att tta gct ttc gta ttt tac gcc ctc atc ctc ggg tca	48
Met Thr Ile Leu Ala Phe Val Phe Tyr Ala Leu Ile Leu Gly Ser	
1 5 10 15	
gta ctc tat gta ttt ctt aac tta agt tca cgt aaa tcc gcc aga ctc	96
Val Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu	
20 25 30	
cca ccc ggg cca aca cca tgg cct ata gtc ggg aac tta cca cac ctt	144
Pro Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu	
35 40 45	
ggc cca atc cca cac cac gca ctc gcg gcc tta gcc aag aag tac ggg	192
Gly Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly	
50 55 60	
cca ttg atg cac ctg cgg ctc ggg tgt gtg gac gtg gtt gtg gcc gcg	240
Pro Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala	
65 70 75	
tct gct tcc gta gct gca cag ttt tta aaa gtt cac gac gca aat ttt	288
Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe	
80 85 90 95	
gct agt agg ccg cca aat tct ggc gcg aaa cat gtg gcg tat aat tat	336
Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr	
100 105 110	
cag gat ctt gtg ttt gca cct tat ggt cca agg tgg cgt ttg tta agg	384
Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg	
115 120 125	
aag att tgt tcg gtc cat ttg ttt tct gct aaa gca ctt gat gat ttt	432
Lys Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe	
130 135 140	
cgt cat gtt cga cag gag gag gta gca gtc cta acc cgc gta cta ctg	480
Arg His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu	
145 150 155	
agt gct gga aac tca ccg gta cag ctt ggc caa cta ctt aac gtg tgt	528
Ser Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys	
160 165 170 175	
gcc aca aac gcc tta gca cgg gta atg tta ggt agg aga gtt ttc gga	576
Ala Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly	
180 185 190	
gac gga att gac agg tca gcc aat gag ttc aaa gat atg gta gta gag	624
Asp Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu	
195 200 205	

tta atg gta tta gca gga gaa ttt aac ctt ggt gac ttt att cct gta	672
Leu Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val	
210 215 220	
ctt gac cta ttc gac cta caa ggc att act aaa aaa atg aag aag ctt	720
Leu Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu	
225 230 235	
cat gtt cgg ttc gat tca ttt ctt agt aag atc gtt gag gag cat aaa	768
His Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys	
240 245 250 255	
acg gca cct ggt ggg ttg ggt cat act gat ttg ctg agc acg ttg att	816
Thr Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile	
260 265 270	
tca ctt aaa gat gat gct gat att gaa ggt ggg aag ctt aca gat act	864
Ser Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr	
275 280 285	
gaa atc aaa gct ttg ctt ctg aat tta ttc gct gcg gga aca gac aca	912
Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr	
290 295 300	
tcc tct agt aca gta gaa tgg gca ata gcc gaa ctc att cgt cat cca	960
Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro	
305 310 315	
caa ata tta aaa caa gcc cga gaa gag ata gac gct gta gtt ggt caa	1008
Gln Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln	
320 325 330 335	
gac cgg ctt gta aca gaa ttg gac ttg agc caa cta aca tac ctc cag	1056
Asp Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln	
340 345 350	
gct ctt gtg aaa gag gtg ttt agg ctc cac cct tca acg cca ctc tcc	1104
Ala Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser	
355 360 365	
tta cca aga ata tca tcc gag agt tgt gag gtc gat ggg tat tat atc	1152
Leu Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile	
370 375 380	
cct aag gga tcc aca ctc ctc gtt aac gtg tgg gcc att gcg cga gac	1200
Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp	
385 390 395	
cca aaa atg tgg gcg gat cct ctt gaa ttt agg cct tct cgg ttt tta	1248
Pro Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu	
400 405 410 415	
ccc ggg gga gaa aag ccc ggt gct gat gtt agg gga aat gat ttt gaa	1296
Pro Gly Gly Glu Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu	
420 425 430	
gtt ata cca ttt ggg gca gga cga agg att tgt gcg ggt atg agc cta	1344
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu	
435 440 445	

ggc ttg aga atg gtc cag ttg ctc att gca aca ttg gtc caa act ttt 1392  
 Gly Leu Arg Met Val Gln Leu Leu Ile Ala Thr Leu Val Gln Thr Phe  
 450 455 460

gat tgg gaa ctg gct aac ggg tta gag ccg gag atg ctc aac atg gaa 1440  
 Asp Trp Glu Leu Ala Asn Gly Leu Glu Pro Glu Met Leu Asn Met Glu  
 465 470 475

gaa gcg tat gga ttg acc ctt caa cgg gct gca ccc ttg atg gtt cac 1488  
 Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His  
 480 485 490 495

ccg aag ccg agg tta gct ccc cac gta tat gaa agt att taa 1530  
 Pro Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile  
 500 505

ggactagtttt ctcttttgcc tttttgtttc gcaaaggtta atgaataaac gatttcatga 1590

ctcagatagt tatgtaaaca attgtgtttg ctgtttatat atttatctat ttttctagaa 1650

caaaaaaaaaa 1660

<210> 17  
 <211> 508  
 <212> PRT  
 <213> Chrysanthemum

<400> 17  
 Met Thr Ile Leu Ala Phe Val Phe Tyr Ala Leu Ile Leu Gly Ser Val  
 1 5 10 15  
 Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu Pro  
 20 25 30  
 Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly  
 35 40 45  
 Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly Pro  
 50 55 60  
 Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala Ser  
 65 70 75 80  
 Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe Ala  
 85 90 95  
 Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln  
 100 105 110  
 Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys  
 115 120 125  
 Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Arg  
 130 135 140  
 His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu Ser  
 145 150 155 160  
 Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys Ala  
 165 170 175  
 Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly Asp  
 180 185 190  
 Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu Leu  
 195 200 205  
 Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val Leu  
 210 215 220  
 Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu His  
 225 230 235 240



Ser	Leu	Arg	Leu	Leu	Leu	Phe	Ser	Gly	Gln	Gly	Arg	Arg	Leu	Leu	Pro		
20					25					30					35		
cca	ggt	cca	cgc	ccg	tgg	ccg	ctg	gtg	gga	aat	ctc	ccg	cac	tta	ggc	259	
Pro	Gly	Pro	Arg	Pro	Trp	Pro	Leu	Val	Gly	Asn	Leu	Pro	His	Leu	Gly		
				40					45					50			
ccg	aag	cca	cac	gcc	tcc	atg	gcc	gag	ctc	gcg	cga	gcc	tac	gga	ccc	307	
Pro	Lys	Pro	His	Ala	Ser	Met	Ala	Glu	Leu	Ala	Arg	Ala	Tyr	Gly	Pro		
			55					60					65				
ctc	atg	cac	cta	aag	atg	ggg	ttc	gtc	cac	gtc	gtg	gtg	gct	tcg	tcg	355	
Leu	Met	His	Leu	Lys	Met	Gly	Phe	Val	His	Val	Val	Val	Ala	Ser	Ser		
		70					75						80				
gcg	agc	gcg	gcg	gag	cag	tgc	ctg	agg	gtt	cac	gac	gcg	aat	ttc	ttg	403	
Ala	Ser	Ala	Ala	Glu	Gln	Cys	Leu	Arg	Val	His	Asp	Ala	Asn	Phe	Leu		
	85					90					95						
agc	agg	cca	ccc	aac	tcc	ggc	gcc	aag	cac	gtc	gct	tac	aac	tac	gag	451	
Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Val	Ala	Tyr	Asn	Tyr	Glu		
100					105					110					115		
gac	ttg	gtt	ttc	aga	ccg	tac	ggg	ccc	aag	tgg	agg	ctg	ttg	agg	aag	499	
Asp	Leu	Val	Phe	Arg	Pro	Tyr	Gly	Pro	Lys	Trp	Arg	Leu	Leu	Arg	Lys		
				120					125					130			
ata	tgc	gct	cag	cat	att	ttc	tcc	gtc	aag	gct	atg	gat	gac	ttc	agg	547	
Ile	Cys	Ala	Gln	His	Ile	Phe	Ser	Val	Lys	Ala	Met	Asp	Asp	Phe	Arg		
			135					140					145				
cgc	gtc	aga	gag	gaa	gag	gtg	gcc	atc	ctg	agt	cgc	gct	cta	gca	ggc	595	
Arg	Val	Arg	Glu	Glu	Glu	Val	Ala	Ile	Leu	Ser	Arg	Ala	Leu	Ala	Gly		
		150					155					160					
aaa	agg	gcc	gta	ccc	ata	ggc	caa	atg	ctc	aac	gtg	tgc	gcc	aca	aac	643	
Lys	Arg	Ala	Val	Pro	Ile	Gly	Gln	Met	Leu	Asn	Val	Cys	Ala	Thr	Asn		
	165					170					175						
gcc	cta	tct	cgc	gtc	atg	atg	ggg	cgg	cgc	gtg	gtg	ggc	cac	gcg	gat	691	
Ala	Leu	Ser	Arg	Val	Met	Met	Gly	Arg	Arg	Val	Val	Gly	His	Ala	Asp		
180					185					190					195		
gga	acc	aac	gac	gcc	aag	gcg	gag	gag	ttc	aaa	gcc	atg	gtc	gtc	gag	739	
Gly	Thr	Asn	Asp	Ala	Lys	Ala	Glu	Glu	Phe	Lys	Ala	Met	Val	Val	Glu		
				200					205					210			
ctc	atg	gtc	ctc	tcc	ggc	gtc	ttc	aac	atc	ggg	gat	ttc	atc	ccc	ttc	787	
Leu	Met	Val	Leu	Ser	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro	Phe		
			215					220					225				
ctc	gag	cct	ctc	gac	ttg	cag	gga	gtg	gct	tcc	aag	atg	aag	aaa	ctc	835	
Leu	Glu	Pro	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	Met	Lys	Lys	Leu		
		230					235					240					
cac	gcg	cgg	ttc	gat	gca	ttc	ttg	acc	gag	att	gta	cga	gag	cgt	tgt	883	
His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Thr	Glu	Ile	Val	Arg	Glu	Arg	Cys		
	245					250					255						

cat ggg cag atc aac aac agt ggt gct cat cag gat gat ttg ctt agc	931
His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp Leu Leu Ser	
260 265 270 275	
acg ttg att tcg ttc aaa ggg ctt gac gat ggc gat ggt tcc agg ctc	979
Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly Ser Arg Leu	
280 285 290	
act gac aca gaa atc aag gcg ctg ctc ttg aac ctt ttg gac acg acg	1027
Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Leu Asp Thr Thr	
295 300 305	
tcg agc acg gtg gaa tgg gcc gta gcc gaa ctc cta cgc cac cct aag	1075
Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg His Pro Lys	
310 315 320	
aca tta gcc caa gtc cgg caa gag ctc gac tcg gtc gtg ggt aag aac	1123
Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val Gly Lys Asn	
325 330 335	
agg ctc gtg tcc gag acc gat ctg aat cag ctg ccc tat cta caa gct	1171
Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr Leu Gln Ala	
340 345 350 355	
gtc gtc aaa gaa act ttc cgc ctc cat cct ccg acg ccg ctc tct cta	1219
Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu	
360 365 370	
ccg aga ctc gcg gaa gat gat tgc gag atc gac gga tac ctc atc ccc	1267
Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr Leu Ile Pro	
375 380 385	
aag ggc tcg acc ctt ctg gtg aac gtt tgg gcc ata gcc cgc gat ccc	1315
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro	
390 395 400	
aag gtt tgg gcc gat ccg ttg gag ttt agg ccc gaa cga ttc ttg acg	1363
Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Leu Thr	
405 410 415	
ggc gga gaa aag gcc gac gtc gat gtc aag ggg aac gat ttc gaa gtg	1411
Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp Phe Glu Val	
420 425 430 435	
ata ccg ttc ggg gcg ggt cgt agg atc tgc gct ggc gtt ggc ttg gga	1459
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val Gly Leu Gly	
440 445 450	
ata cgt atg gtc caa ctg ttg acg gcg agt ttg atc cat gca ttc gat	1507
Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His Ala Phe Asp	
455 460 465	
ctg gac ctt gct aat ggg ctt ttg gcc caa aat ctg aac atg gaa gaa	1555
Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn Met Glu Glu	
470 475 480	
gca tat ggg ctt acg cta caa cgg gct gag cct ttg ttg gtc cac cct	1603
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu Val His Pro	
485 490 495	



agg ccg cgg ttg gcc act cat gtc tat taa ttaaattagg cctaaactac 1653  
 Arg Pro Arg Leu Ala Thr His Val Tyr  
 500 505

gatgaatgac ccatttaacg ttaataagag ttttcaattt atgtgagttt gcatgggtatg 1713

gtatgggtatg gtgcttgtaa taaattgtat ctggttaggtg tgttcattga tgataaatct 1773

agtttgtact gctgctcaaa aaaaaaaaaa aaaaaaaaaa aa 1815

<210> 19  
 <211> 508  
 <212> PRT  
 <213> Torenia

<400> 19  
 Met Ser Pro Leu Ala Leu Met Ile Ile Ser Thr Leu Leu Gly Phe Leu  
 1 5 10 15  
 Leu Tyr His Ser Leu Arg Leu Leu Leu Phe Ser Gly Gln Gly Arg Arg  
 20 25 30  
 Leu Leu Pro Pro Gly Pro Arg Pro Trp Pro Leu Val Gly Asn Leu Pro  
 35 40 45  
 His Leu Gly Pro Lys Pro His Ala Ser Met Ala Glu Leu Ala Arg Ala  
 50 55 60  
 Tyr Gly Pro Leu Met His Leu Lys Met Gly Phe Val His Val Val Val  
 65 70 75 80  
 Ala Ser Ser Ala Ser Ala Ala Glu Gln Cys Leu Arg Val His Asp Ala  
 85 90 95  
 Asn Phe Leu Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr  
 100 105 110  
 Asn Tyr Glu Asp Leu Val Phe Arg Pro Tyr Gly Pro Lys Trp Arg Leu  
 115 120 125  
 Leu Arg Lys Ile Cys Ala Gln His Ile Phe Ser Val Lys Ala Met Asp  
 130 135 140  
 Asp Phe Arg Arg Val Arg Glu Glu Glu Val Ala Ile Leu Ser Arg Ala  
 145 150 155 160  
 Leu Ala Gly Lys Arg Ala Val Pro Ile Gly Gln Met Leu Asn Val Cys  
 165 170 175  
 Ala Thr Asn Ala Leu Ser Arg Val Met Met Gly Arg Arg Val Val Gly  
 180 185 190  
 His Ala Asp Gly Thr Asn Asp Ala Lys Ala Glu Glu Phe Lys Ala Met  
 195 200 205  
 Val Val Glu Leu Met Val Leu Ser Gly Val Phe Asn Ile Gly Asp Phe  
 210 215 220  
 Ile Pro Phe Leu Glu Pro Leu Asp Leu Gln Gly Val Ala Ser Lys Met  
 225 230 235 240  
 Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Glu Ile Val Arg  
 245 250 255  
 Glu Arg Cys His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp  
 260 265 270  
 Leu Leu Ser Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly  
 275 280 285  
 Ser Arg Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Leu  
 290 295 300  
 Asp Thr Thr Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg  
 305 310 315 320  
 His Pro Lys Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val  
 325 330 335

Gly Lys Asn Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr  
                   340                  345                  350  
 Leu Gln Ala Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro  
                   355                  360                  365  
 Leu Ser Leu Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr  
                   370                  375                  380  
 Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala  
 385                  390                  395                  400  
 Arg Asp Pro Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg  
                   405                  410                  415  
 Phe Leu Thr Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp  
                   420                  425                  430  
 Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val  
                   435                  440                  445  
 Gly Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His  
                   450                  455                  460  
 Ala Phe Asp Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn  
 465                  470                  475                  480  
 Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu  
                   485                  490                  495  
 Val His Pro Arg Pro Arg Leu Ala Thr His Val Tyr  
                   500                  505

<210> 20  
 <211> 1824  
 <212> DNA  
 <213> Jap. Morning Glory

<220>  
 <221> CDS  
 <222> (2)..(1555)

<400> 20  
 g agc tta acc tta att ttc tgc act tta gtt ttt gca atc ttt cta tat 49  
   Ser Leu Thr Leu Ile Phe Cys Thr Leu Val Phe Ala Ile Phe Leu Tyr  
       1                  5                  10                  15  
  
 ttt ctt att ctc agg gtg aaa cag cgt tac cct tta cct ctc cca ccc 97  
 Phe Leu Ile Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro Pro  
                   20                  25                  30  
  
 gga cca aaa cca tgg ccg gtg tta gga aac ctt ccc cac ctg ggc aag 145  
 Gly Pro Lys Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly Lys  
                   35                  40                  45  
  
 aag cct cac cag tcg att gcg gcc atg gct gag agg tac ggc ccc ctc 193  
 Lys Pro His Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro Leu  
                   50                  55                  60  
  
 atg cac ctc cgc cta gga ttc gtg gac gtg gtt gtg gcc gcc tcc gcc 241  
 Met His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala Ala Ser Ala  
                   65                  70                  75                  80  
  
 gcc gtg gcc gct cag ttc ttg aaa gtt cac gac tcg aac ttc tcc aac 289  
 Ala Val Ala Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser Asn  
                   85                  90                  95  
  
 cgg ccg ccg aac tcc ggc gcg gaa cac att gct tat aac tat caa gac 337

Arg	Pro	Pro	Asn	Ser	Gly	Ala	Glu	His	Ile	Ala	Tyr	Asn	Tyr	Gln	Asp		
			100					105					110				
ctc	gtc	ttc	gcg	ccc	tac	ggc	ccg	cgg	tgg	cgc	atg	ctt	agg	aag	atc	385	
Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Leu	Arg	Lys	Ile		
		115					120					125					
acc	tcc	gtg	cat	ctc	ttc	tcg	gcc	aag	gcg	ttg	gat	gac	ttc	tgc	cat	433	
Thr	Ser	Val	His	Leu	Phe	Ser	Ala	Lys	Ala	Leu	Asp	Asp	Phe	Cys	His		
	130					135					140						
gtt	cgc	cag	gaa	gag	gtt	gca	act	ctg	aca	cgc	agt	cta	gca	agt	gca	481	
Val	Arg	Gln	Glu	Glu	Val	Ala	Thr	Leu	Thr	Arg	Ser	Leu	Ala	Ser	Ala		
145					150					155					160		
ggc	aaa	act	cca	gta	aaa	cta	ggg	cag	tta	cta	aac	gtg	tgc	acc	acg	529	
Gly	Lys	Thr	Pro	Val	Lys	Leu	Gly	Gln	Leu	Leu	Asn	Val	Cys	Thr	Thr		
			165					170						175			
aac	gcc	cta	gct	cgt	gta	atg	cta	ggg	cgg	aag	gtc	ttt	aat	gac	gga	577	
Asn	Ala	Leu	Ala	Arg	Val	Met	Leu	Gly	Arg	Lys	Val	Phe	Asn	Asp	Gly		
			180					185					190				
ggt	agc	aag	agc	gac	cca	aag	gcg	gag	gag	ttc	aag	tcg	atg	gtg	gag	625	
Gly	Ser	Lys	Ser	Asp	Pro	Lys	Ala	Glu	Glu	Phe	Lys	Ser	Met	Val	Glu		
		195					200					205					
gag	atg	atg	gtg	ttg	gcc	gga	agt	ttt	aac	atc	ggc	gat	ttc	att	ccg	673	
Glu	Met	Met	Val	Leu	Ala	Gly	Ser	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro		
	210					215					220						
gtc	ttg	ggt	tgg	ttt	gac	gtt	cag	ggt	atc	gta	ggg	aag	atg	aag	aaa	721	
Val	Leu	Gly	Trp	Phe	Asp	Val	Gln	Gly	Ile	Val	Gly	Lys	Met	Lys	Lys		
225					230					235					240		
cta	cac	gcg	cgt	ttt	gat	gcg	ttc	ttg	aac	acc	att	cta	gag	gaa	cac	769	
Leu	His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Asn	Thr	Ile	Leu	Glu	Glu	His		
				245					250					255			
aaa	tgt	gtc	aac	aat	caa	cac	acg	acg	ttg	tcg	aaa	gat	gtg	gac	ttc	817	
Lys	Cys	Val	Asn	Asn	Gln	His	Thr	Thr	Leu	Ser	Lys	Asp	Val	Asp	Phe		
			260					265					270				
ttg	agc	acc	cta	att	agg	ctc	aaa	gat	aat	ggg	gct	gat	atg	gat	tgt	865	
Leu	Ser	Thr	Leu	Ile	Arg	Leu	Lys	Asp	Asn	Gly	Ala	Asp	Met	Asp	Cys		
		275					280					285					
gaa	gag	gga	aaa	ctc	acc	gac	act	gaa	att	aag	gct	ttg	ctc	ttg	aac	913	
Glu	Glu	Gly	Lys	Leu	Thr	Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn		
		290				295					300						
ctg	ttc	aca	gct	ggg	act	gat	aca	tca	tct	agc	act	gtg	gag	tgg	gca	961	
Leu	Phe	Thr	Ala	Gly	Thr	Asp	Thr	Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala		
305					310					315					320		
atc	gca	gaa	cta	cta	cgc	aac	cca	aaa	atc	tta	aac	caa	gca	caa	caa	1009	
Ile	Ala	Glu	Leu	Leu	Arg	Asn	Pro	Lys	Ile	Leu	Asn	Gln	Ala	Gln	Gln		
				325					330					335			
gag	ctt	gac	tta	gtg	gtg	ggt	caa	aat	cag	cta	gtc	aca	gaa	tct	gac	1057	

Glu	Leu	Asp	Leu	Val	Val	Gly	Gln	Asn	Gln	Leu	Val	Thr	Glu	Ser	Asp	
			340					345					350			
tta	acc	gat	cta	cct	ttc	ctg	caa	gca	ata	gtg	aag	gag	acc	ttc	agg	1105
Leu	Thr	Asp	Leu	Pro	Phe	Leu	Gln	Ala	Ile	Val	Lys	Glu	Thr	Phe	Arg	
		355				360					365					
cta	cac	cca	tcc	acc	cca	ctc	tct	ctt	cca	aga	atg	gga	gct	cag	ggt	1153
Leu	His	Pro	Ser	Thr	Pro	Leu	Ser	Leu	Pro	Arg	Met	Gly	Ala	Gln	Gly	
	370					375					380					
tgc	gag	atc	aat	ggc	tac	ttc	atc	ccc	aaa	ggc	gca	acg	ctt	ttg	gtc	1201
Cys	Glu	Ile	Asn	Gly	Tyr	Phe	Ile	Pro	Lys	Gly	Ala	Thr	Leu	Leu	Val	
385				390						395					400	
aac	gtt	tgg	gcc	ata	gct	cgt	gat	ccc	aat	gtg	tgg	aca	aat	cct	ctt	1249
Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro	Asn	Val	Trp	Thr	Asn	Pro	Leu	
			405					410						415		
gag	ttc	aac	cca	cac	cga	ttc	ttg	cct	ggg	gga	gaa	aag	ccc	aac	gtg	1297
Glu	Phe	Asn	Pro	His	Arg	Phe	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Asn	Val	
		420						425					430			
gat	att	aaa	ggg	aat	gac	ttt	gaa	gtg	att	cct	ttt	gga	gcc	ggg	cgt	1345
Asp	Ile	Lys	Gly	Asn	Asp	Phe	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	
		435					440					445				
aga	ata	tgc	tct	ggg	atg	agt	ttg	ggg	ata	agg	atg	gtt	cac	ctg	ttg	1393
Arg	Ile	Cys	Ser	Gly	Met	Ser	Leu	Gly	Ile	Arg	Met	Val	His	Leu	Leu	
	450					455					460					
gtt	gca	act	ttg	gtg	cat	gct	ttt	gat	tgg	gat	ttg	gtg	aat	gga	caa	1441
Val	Ala	Thr	Leu	Val	His	Ala	Phe	Asp	Trp	Asp	Leu	Val	Asn	Gly	Gln	
465					470					475					480	
tct	gta	gag	acg	ctc	aat	atg	gag	gaa	gct	tat	ggg	ctc	acc	ctt	caa	1489
Ser	Val	Glu	Thr	Leu	Asn	Met	Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	
				485					490					495		
cga	gct	gtt	cct	ttg	atg	ttg	cat	cca	aag	ccc	aga	tta	caa	cca	cat	1537
Arg	Ala	Val	Pro	Leu	Met	Leu	His	Pro	Lys	Pro	Arg	Leu	Gln	Pro	His	
		500						505					510			
ctc	tat	act	ctc	aat	taa	attgcaattt	gatttttggtg	attataacaat								1585
Leu	Tyr	Thr	Leu	Asn												
		515														
tataatcgag	ggacatagga	tccccattta	tttatattca	gttataagag	acttccaaca											1645
aaggtctagc	tttcgacctt	aaaagttgta	aaagaggtcc	tacatatgta	aaagccccgcc											1705
aaaggaaaac	tggttgtatt	caattccgct	aggccttgtc	cgaaagacct	catgaagact											1765
acaaaggtca	tatataatgg	taaaccagct	gtatttggtg	taaaaaaaaa	aaaaaaaaaa											1824

<210> 21  
 <211> 517  
 <212> PRT

<400> 21

37

Arg Ile Cys Ser Gly Met Ser Leu Gly Ile Arg Met Val His Leu Leu  
 450 455 460  
 Val Ala Thr Leu Val His Ala Phe Asp Trp Asp Leu Val Asn Gly Gln  
 465 470 475 480  
 Ser Val Glu Thr Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln  
 485 490 495  
 Arg Ala Val Pro Leu Met Leu His Pro Lys Pro Arg Leu Gln Pro His  
 500 505 510  
 Leu Tyr Thr Leu Asn  
 515

<210> 22  
 <211> 1667  
 <212> DNA  
 <213> Gentian

<220>  
 <221> CDS  
 <222> (1)..(1431)

<400> 22  
 ccc atc ctc gga aac atc ccc cat ctc ggc tcc aaa ccg cac caa aca 48  
 Pro Ile Leu Gly Asn Ile Pro His Leu Gly Ser Lys Pro His Gln Thr  
 1 5 10 15  
 ctc gcg gaa atg gcg aaa acc tac ggt ccg ctc atg cac ttg aag ttc 96  
 Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe  
 20 25 30  
 ggg ctt aag gac gcg gtg gtg gcg tcg tct gcg tcg gtg gca gag cag 144  
 Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln  
 35 40 45  
 ttt ctg aag aaa cac gac gtg aat ttc tcg aac cgg ccg cca aac tcc 192  
 Phe Leu Lys Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser  
 50 55 60  
 ggg gcc aaa cat ata gct tat aac tat cag gac ctg gta ttc gct ccc 240  
 Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro  
 65 70 75 80  
 tat gga ccc ccg tgg ccg ttg ctt agg aaa atc tgt tcc gtc cat ctt 288  
 Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu  
 85 90 95  
 ttc tcg tct aag gcc ttg gat gac ttt cag cat gtt cga cat gag gag 336  
 Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu  
 100 105 110  
 ata tgc atc ctt ata cga gca ata gcg agt ggc ggt cat gct ccg gtg 384  
 Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val  
 115 120 125  
 aat tta ggc aag tta tta gga gtg tgc aca acc aat gcc ctg gca aga 432  
 Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg  
 130 135 140  
 gtg atg ctt gga aga aga gta ttc gaa ggc gac ggc ggc gag aat ccg 480

Val	Met	Leu	Gly	Arg	Arg	Val	Phe	Glu	Gly	Asp	Gly	Gly	Glu	Asn	Pro		
145					150					155					160		
cat	gcc	gac	gag	ttt	aaa	tca	atg	gtg	gtg	gag	att	atg	gtg	tta	gcc	528	
His	Ala	Asp	Glu	Phe	Lys	Ser	Met	Val	Val	Glu	Ile	Met	Val	Leu	Ala		
				165					170					175			
ggt	gca	ttc	aac	ttg	ggt	gat	ttc	atc	ccg	gtt	cta	gat	tgg	ttc	gat	576	
Gly	Ala	Phe	Asn	Leu	Gly	Asp	Phe	Ile	Pro	Val	Leu	Asp	Trp	Phe	Asp		
			180					185					190				
ttg	caa	gga	att	gct	ggt	aaa	atg	aag	aaa	ctt	cat	gcc	cgt	ttc	gac	624	
Leu	Gln	Gly	Ile	Ala	Gly	Lys	Met	Lys	Lys	Leu	His	Ala	Arg	Phe	Asp		
			195				200					205					
aag	ttt	tta	aat	ggg	atc	cta	gaa	gat	cgt	aaa	tct	aac	ggc	tct	aat	672	
Lys	Phe	Leu	Asn	Gly	Ile	Leu	Glu	Asp	Arg	Lys	Ser	Asn	Gly	Ser	Asn		
	210					215					220						
gga	gct	gaa	caa	tac	gtg	gac	ttg	ctc	agt	gtg	ttg	atc	tct	ctt	caa	720	
Gly	Ala	Glu	Gln	Tyr	Val	Asp	Leu	Leu	Ser	Val	Leu	Ile	Ser	Leu	Gln		
225					230					235					240		
gat	agt	aat	atc	gac	ggt	ggt	gac	gaa	gga	acc	aaa	ctc	aca	gat	act	768	
Asp	Ser	Asn	Ile	Asp	Gly	Gly	Asp	Glu	Gly	Thr	Lys	Leu	Thr	Asp	Thr		
				245					250					255			
gaa	atc	aaa	gct	ctc	ctt	ttg	aac	ttg	ttc	ata	gcc	gga	aca	gac	act	816	
Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Ile	Ala	Gly	Thr	Asp	Thr		
			260					265					270				
tca	tca	agt	act	gta	gaa	tgg	gcc	atg	gca	gaa	cta	atc	cga	aac	cca	864	
Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Met	Ala	Glu	Leu	Ile	Arg	Asn	Pro		
			275				280						285				
aag	tta	cta	gtc	caa	gcc	caa	gaa	gag	cta	gac	aga	gta	gtc	ggg	ccg	912	
Lys	Leu	Leu	Val	Gln	Ala	Gln	Glu	Glu	Leu	Asp	Arg	Val	Val	Gly	Pro		
	290					295					300						
aac	cga	ttc	gta	acc	gaa	tct	gat	ctt	cct	caa	ctg	aca	ttc	ctt	caa	960	
Asn	Arg	Phe	Val	Thr	Glu	Ser	Asp	Leu	Pro	Gln	Leu	Thr	Phe	Leu	Gln		
305					310					315					320		
gcc	gtc	atc	aaa	gag	act	ttc	agg	ctt	cat	cca	tcc	acc	cca	ctc	tct	1008	
Ala	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser		
				325					330					335			
ctt	cca	cga	atg	gcg	gcg	gag	gac	tgt	gag	atc	aat	ggg	tat	tat	gtc	1056	
Leu	Pro	Arg	Met	Ala	Ala	Glu	Asp	Cys	Glu	Ile	Asn	Gly	Tyr	Tyr	Val		
			340					345					350				
tca	gaa	ggt	tcg	aca	ttg	ctc	gtc	aat	gtg	tgg	gcc	ata	gct	cgt	gat	1104	
Ser	Glu	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp		
			355				360					365					
cca	aat	gcg	tgg	gcc	aat	cca	cta	gat	ttc	aac	ccg	act	cgt	ttc	ttg	1152	
Pro	Asn	Ala	Trp	Ala	Asn	Pro	Leu	Asp	Phe	Asn	Pro	Thr	Arg	Phe	Leu		
	370					375					380						
gcc	ggt	gga	gag	aag	cct	aat	gtt	gat	gtt	aaa	ggg	aat	gat	ttt	gaa	1200	

Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu  
385 390 395 400

gtg ata cct ttc ggt gct ggg cgc agg ata tgt gcc gga atg agc tta 1248  
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu  
405 410 415

ggt ata cgg atg gtt caa cta gta acg gct tcg tta gtt cat tcg ttt 1296  
Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe  
420 425 430

gat tgg gct ttg ttg gat gga ctt aaa ccc gag aag ctt gac atg gag 1344  
Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu  
435 440 445

gaa ggt tat gga cta acg ctt caa cga gct tca cct tta atc gtc cat 1392  
Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His  
450 455 460

cca aag ccg agg ctc tcg gct caa gtt tat tgt atg taa caagtttgtg 1441  
Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met  
465 470 475

aagccagtct gatttcagtt ggattttag ttattttatg atcatttggt attttatttt 1501

gtatttcggt tgaatacaat aaaggaagg tggatcgtct gctgtataat agcgacgttt 1561

taacgtgttg tgatagtacc gtgttttact aaaacgatgt cgtttgattt tttatagtat 1621

taaaaaaata aacagctgga ttttgaacca aaaaaaaaaa aaaaaa 1667

<210> 23  
<211> 476  
<212> PRT  
<213> Gentian

<400> 23

Pro Ile Leu Gly Asn Ile Pro His Leu Gly Ser Lys Pro His Gln Thr  
1 5 10 15

Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe  
20 25 30

Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln  
35 40 45

Phe Leu Lys Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser  
50 55 60

Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro  
65 70 75 80

Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu  
85 90 95

Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu  
100 105 110

Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val  
115 120 125

Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg  
130 135 140

Val Met Leu Gly Arg Arg Val Phe Glu Gly Asp Gly Gly Glu Asn Pro  
145 150 155 160

His Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala





atg ctt gga agg agg gta ttc ggc gat ggg agc ggc ggc gta gat cct	145
Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro	
35 40 45	
cag gcg gac gag ttc aaa tcc atg gtg gtg gaa atc atg gtg ttg gcc	193
Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala	
50 55 60	
ggc gcg ttt aat cta ggt gat ttt att ccc gct ctt gat tgg ttc gat	241
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp	
65 70 75 80	
ctg cag gga att acg gca aaa atg aag aaa gtt cac gct cgt ttc gat	289
Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp	
85 90 95	
gcg ttc tta gac gcg atc ctt gag gag cac aaa tcc aac ggc tct cgc	337
Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg	
100 105 110	
gga gct aag caa cac gtt gac ttg ctg agt atg ttg atc tcc ctt caa	385
Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln	
115 120 125	
gat aat aac att gat ggt gaa agt ggc gcc aaa ctc act gat aca gaa	433
Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu	
130 135 140	
atc aaa gct ttg ctt ctg aac ttg ttc acg gct gga aca gac acg tca	481
Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser	
145 150 155 160	
tca agt act gtg gag tgg gca atc gca gag cta atc cga aac cca gaa	529
Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu	
165 170 175	
gta ttg gtt caa gcc caa caa gag ctc gat aga gta gtt ggg cca agt	577
Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser	
180 185 190	
cgt ctt gtg acc gaa tct gat ctg cct caa ttg gca ttc ctt caa gct	625
Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala	
195 200 205	
gtc atc aaa gag act ttc aga ctt cat cca tcc act cca ctc tct ctt	673
Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu	
210 215 220	
cca cga atg gct tca gag ggt tgt gaa atc aat gga tac tcc atc cca	721
Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro	
225 230 235 240	
aag ggt tcg aca ttg ctc gtt aac gta tgg tcc ata gcc cgt gat cct	769
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro	
245 250 255	
agt ata tgg gcc gac cca tta gaa ttt agg ccg gca cgt ttc ttg ccc	817
Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro	
260 265 270	

ggc gga gaa aag ccc aat gtt gat gtg aga ggc aat gat ttt gag gtc 865  
 Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val  
 275 280 285  
 ata cca ttt ggt gct gga cgt agg ata tgt gct gga atg agc ttg ggt 913  
 Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly  
 290 295 300  
 tta aga atg gtt caa ctt tcg aca gct act ttg gtt cat tcg ttt aat 961  
 Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn  
 305 310 315 320  
 tgg gat ttg ctg aat ggg atg agc cca gat aaa ctt gac atg gaa gaa 1009  
 Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu  
 325 330 335  
 gct tat ggg ctt aca ttg caa cgg gct tca cct ttg att gtc cac cca 1057  
 Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro  
 340 345 350  
 aag ccc agg ctt gct agc tct atg tat gtt aaa tga aattatgctg 1103  
 Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys  
 355 360  
 tgcgaataat tccttattta tagcaggaaa tgatcatcttg aattatgtgt aatgttcttc 1163  
 taactttcga tggaagtgc aaacaagttt tattaaaaaa aaaaaaaaaa a 1214

<210> 25  
 <211> 363  
 <212> PRT  
 <213> Lisianthus

<400> 25  
 Arg Ile Leu Thr Arg Ser Ile Ala Ser Ala Gly Glu Asn Pro Ile Asn  
 1 5 10 15  
 Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg Val  
 20 25 30  
 Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro  
 35 40 45  
 Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala  
 50 55 60  
 Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp  
 65 70 75 80  
 Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp  
 85 90 95  
 Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg  
 100 105 110  
 Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln  
 115 120 125  
 Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu  
 130 135 140  
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser  
 145 150 155 160  
 Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu  
 165 170 175  
 Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser  
 180 185 190  
 Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala

195	200	205
Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu		
210	215	220
Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro		
225	230	235
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro		
245	250	255
Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro		
260	265	270
Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val		
275	280	285
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly		
290	295	300
Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn		
305	310	315
Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu		
325	330	335
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro		
340	345	350
Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys		
355	360	

<210> 26  
 <211> 1757  
 <212> DNA  
 <213> Petunia sp.

<220>  
 <221> CDS  
 <222> (35)..(1525)

<400> 26  
 ccgttgctgt cgagaaaaca gaaagaagag aaaa atg gac tac gtg aat att ttg 55  
 Met Asp Tyr Val Asn Ile Leu  
 1 5

ctg gga ctg ttt ttc act tgg ttc ttg gtg aat gga ctc atg tca ctt 103  
 Leu Gly Leu Phe Phe Thr Trp Phe Leu Val Asn Gly Leu Met Ser Leu  
 10 15 20

cga aga aga aaa atc tct aag aaa ctt cca cca ggt cca ttt cct ttg 151  
 Arg Arg Arg Lys Ile Ser Lys Lys Leu Pro Pro Gly Pro Phe Pro Leu  
 25 30 35

cct atc atc gga aat ctt cac tta ctt ggt aat cat cct cac aaa tca 199  
 Pro Ile Ile Gly Asn Leu His Leu Leu Gly Asn His Pro His Lys Ser  
 40 45 50 55

ctt gct caa ctt gca aaa att cat ggt cct att atg aat ctc aaa tta 247  
 Leu Ala Gln Leu Ala Lys Ile His Gly Pro Ile Met Asn Leu Lys Leu  
 60 65 70

ggc caa cta aac aca gtg gtc att tca tca tca gtc gtg gca aga gaa 295  
 Gly Gln Leu Asn Thr Val Val Ile Ser Ser Ser Val Val Ala Arg Glu  
 75 80 85

gtc ttg caa aaa caa gac tta aca ttt tcc aat agg ttt gtc ccg gac 343  
 Val Leu Gln Lys Gln Asp Leu Thr Phe Ser Asn Arg Phe Val Pro Asp

90	95	100	
gta gtc cat gtc cga aat cac tcc gat ttt tct gtt gtt tgg tta cca Val Val His Val Arg Asn His Ser Asp Phe Ser Val Val Trp Leu Pro 105 110 115			391
gtc aat tct cga tgg aaa acg ctt cgc aaa atc atg aac tct agc atc Val Asn Ser Arg Trp Lys Thr Leu Arg Lys Ile Met Asn Ser Ser Ile 120 125 130 135			439
ttt tct ggt aac aag ctt gat ggt aat caa cat ctg agg tct aaa aag Phe Ser Gly Asn Lys Leu Asp Gly Asn Gln His Leu Arg Ser Lys Lys 140 145 150			487
gtc caa gag tta att gat tat tgt caa aag tgt gcc aag aat ggc gaa Val Gln Glu Leu Ile Asp Tyr Cys Gln Lys Cys Ala Lys Asn Gly Glu 155 160 165			535
gca gtg gat ata gga aga gca act ttt gga act act ttg aat ttg cta Ala Val Asp Ile Gly Arg Ala Thr Phe Gly Thr Thr Leu Asn Leu Leu 170 175 180			583
tcc aac acc att ttc tct aaa gat ttg act aat ccg ttt tct gat tct Ser Asn Thr Ile Phe Ser Lys Asp Leu Thr Asn Pro Phe Ser Asp Ser 185 190 195			631
gct aaa gag ttt aag gaa ttg gtt tgg aac att atg gtt gag gct gga Ala Lys Glu Phe Lys Glu Leu Val Trp Asn Ile Met Val Glu Ala Gly 200 205 210 215			679
aaa ccc aat ttg gtg gac tac ttt cct ttc ctt gag aaa att gat ccg Lys Pro Asn Leu Val Asp Tyr Phe Pro Phe Leu Glu Lys Ile Asp Pro 220 225 230			727
caa ggt ata aag cga cgc atg act aat aat ttt act aag ttt ctt ggc Gln Gly Ile Lys Arg Arg Met Thr Asn Asn Phe Thr Lys Phe Leu Gly 235 240 245			775
ctt atc agc ggt ttg att gat gac cgg tta aag gaa agg aat cta agg Leu Ile Ser Gly Leu Ile Asp Asp Arg Leu Lys Glu Arg Asn Leu Arg 250 255 260			823
gac aat gca aat att gat gtt tta gac gcc ctt ctc aac att agc caa Asp Asn Ala Asn Ile Asp Val Leu Asp Ala Leu Leu Asn Ile Ser Gln 265 270 275			871
gag aac cca gaa gag att gac agg aat caa atc gag cag ttg tgt ctg Glu Asn Pro Glu Glu Ile Asp Arg Asn Gln Ile Glu Gln Leu Cys Leu 280 285 290 295			919
gac ttg ttt gca gca ggg act gat act aca tcg aat acc ttg gag tgg Asp Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Asn Thr Leu Glu Trp 300 305 310			967
gca atg gca gaa cta ctt cag aat cca cac aca ttg cag aaa gca caa Ala Met Ala Glu Leu Leu Gln Asn Pro His Thr Leu Gln Lys Ala Gln 315 320 325			1015
gaa gaa ctt gca caa gtc att ggt aaa ggc aaa caa gta gaa gaa gca Glu Glu Leu Ala Gln Val Ile Gly Lys Gly Lys Gln Val Glu Glu Ala 1063			

330	335	340	
gat gtt gga cga cta cct tac ttg cga tgc ata gtg aaa gaa acc tta Asp Val Gly Arg Leu Pro Tyr Leu Arg Cys Ile Val Lys Glu Thr Leu 345 350 355			1111
cga ata cac cca gcg gct cct ctc tta att cca cgt aaa gtg gag gaa Arg Ile His Pro Ala Ala Pro Leu Leu Ile Pro Arg Lys Val Glu Glu 360 365 370 375			1159
gac gtt gag ttg tct acc tat att att cca aag gat tca caa gtt cta Asp Val Glu Leu Ser Thr Tyr Ile Ile Pro Lys Asp Ser Gln Val Leu 380 385 390			1207
gtg aac gta tgg gca att gga cgc aac tct gat cta tgg gaa aat cct Val Asn Val Trp Ala Ile Gly Arg Asn Ser Asp Leu Trp Glu Asn Pro 395 400 405			1255
ttg gtc ttt aag cca gaa agg ttt tgg gag tca gaa ata gat atc cga Leu Val Phe Lys Pro Glu Arg Phe Trp Glu Ser Glu Ile Asp Ile Arg 410 415 420			1303
ggt cga gat ttt gaa ctc att cca ttt ggt gct ggt cga aga att tgc Gly Arg Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys 425 430 435			1351
cct gga ttg cct ttg gct atg agg atg att cca gta gca cta ggt tca Pro Gly Leu Pro Leu Ala Met Arg Met Ile Pro Val Ala Leu Gly Ser 440 445 450 455			1399
ttg cta aac tca ttt aat tgg aaa cta tat ggt gga att gca cct aaa Leu Leu Asn Ser Phe Asn Trp Lys Leu Tyr Gly Gly Ile Ala Pro Lys 460 465 470			1447
gat ttg gac atg cag gaa aag ttt ggc att acc ttg gcg aaa gcc caa Asp Leu Asp Met Gln Glu Lys Phe Gly Ile Thr Leu Ala Lys Ala Gln 475 480 485			1495
cct ctg cta gct atc cca act ccc ctg tag ctatagggat aaattaagtt Pro Leu Leu Ala Ile Pro Thr Pro Leu 490 495			1545
gagggttttaa gttactagta gattctattg cagctatagg atttctttca ccatacagta			1605
tgctttaccg ttggatgatg gaaagaaata tctatagctt tgggtttggt tagtttgcac			1665
ataaaaaattg aatgaatgga ataccatgga gttataagaa ataataagac tatgattctt			1725
accctacttg aacaatgaca tggctatttc ac			1757

<210> 27

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> 27  
tttttttttt ttttttta

18

<210> 28  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 28  
tttttttttt tttttttc

18

<210> 29  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 29  
tttttttttt tttttttg

18

<210> 30  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 30  
Trp Ala Ile Gly Arg Asp Pro  
1 5

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
<221> Modified Base  
<222> (6)  
<223> n is inosine

<220>  
<221> Modified Base  
<222> (9)  
<223> n is inosine

<220>  
<221> Modified Base  
<222> (12)  
<223> n is inosine

<220>  
<221> Modified Base  
<222> (15)  
<223> n is inosine

<400> 31  
tgggcnatng gnmngaycc

20

<210> 32  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 32  
Phe Arg Pro Glu Arg Phe  
1 5

<210> 33  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: oligonucleotide

<220>  
<221> Modified base  
<222> (11)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (14)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (20)  
<223> n is inosine

<400> 33  
aggaattymg nccngarmgn tt

22

<210> 34  
<211> 32  
<212> DNA  
<213> Artificial Sequence



<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
<221> Modified base  
<222> (3)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (9)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (12)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (15)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (18)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (21)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (24)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (30)  
<223> n is inosine

<400> 34  
ccnttyggng cnggnmgng natntgkscn gg

32

<210> 35  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<220>  
<221> UNSURE  
<222> (3)  
<223> Xaa can be any amino acid.

<400> 35  
Glu Phe Xaa Pro Glu Arg Phe  
1 5

<210> 36  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
<221> Modified base  
<222> (3)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (7)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (8)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (9)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (12)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (15)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (18)  
<223> n is inosine

<400> 36  
ganttynnnc cnganmgntt

20

<210> 37  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 37  
ccacacgagt agttttggca ttgaccc

28

<210> 38  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 38  
gtcttggaca tcacacttca atctg

25

<210> 39  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 39  
ccgaattccc cccccc

17

<210> 40  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
<221> Modified base  
<222> (3)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (9)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (12)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (18)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (21)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (24)  
<223> n is inosine

<220>  
 <221> Modified base  
 <222> (30)  
 <223> n is inosine

<400> 40  
 ccnggrcana tncyytncc ngcnccraan gg

32

<210> 41  
 <211> 496  
 <212> PRT  
 <213> Petunia sp.

<400> 41

Met	Asp	Tyr	Val	Asn	Ile	Leu	Leu	Gly	Leu	Phe	Phe	Thr	Trp	Phe	Leu
1				5					10					15	
Val	Asn	Gly	Leu	Met	Ser	Leu	Arg	Arg	Arg	Lys	Ile	Ser	Lys	Lys	Leu
		20						25					30		
Pro	Pro	Gly	Pro	Phe	Pro	Leu	Pro	Ile	Ile	Gly	Asn	Leu	His	Leu	Leu
		35					40					45			
Gly	Asn	His	Pro	His	Lys	Ser	Leu	Ala	Gln	Leu	Ala	Lys	Ile	His	Gly
	50					55					60				
Pro	Ile	Met	Asn	Leu	Lys	Leu	Gly	Gln	Leu	Asn	Thr	Val	Val	Ile	Ser
65					70					75					80
Ser	Ser	Val	Val	Ala	Arg	Glu	Val	Leu	Gln	Lys	Gln	Asp	Leu	Thr	Phe
				85					90					95	
Ser	Asn	Arg	Phe	Val	Pro	Asp	Val	Val	His	Val	Arg	Asn	His	Ser	Asp
			100					105					110		
Phe	Ser	Val	Val	Trp	Leu	Pro	Val	Asn	Ser	Arg	Trp	Lys	Thr	Leu	Arg
		115					120					125			
Lys	Ile	Met	Asn	Ser	Ser	Ile	Phe	Ser	Gly	Asn	Lys	Leu	Asp	Gly	Asn
	130					135					140				
Gln	His	Leu	Arg	Ser	Lys	Lys	Val	Gln	Glu	Leu	Ile	Asp	Tyr	Cys	Gln
145					150					155					160
Lys	Cys	Ala	Lys	Asn	Gly	Glu	Ala	Val	Asp	Ile	Gly	Arg	Ala	Thr	Phe
			165						170					175	
Gly	Thr	Thr	Leu	Asn	Leu	Leu	Ser	Asn	Thr	Ile	Phe	Ser	Lys	Asp	Leu
			180					185					190		
Thr	Asn	Pro	Phe	Ser	Asp	Ser	Ala	Lys	Glu	Phe	Lys	Glu	Leu	Val	Trp
		195					200					205			
Asn	Ile	Met	Val	Glu	Ala	Gly	Lys	Pro	Asn	Leu	Val	Asp	Tyr	Phe	Pro
	210					215					220				
Phe	Leu	Glu	Lys	Ile	Asp	Pro	Gln	Gly	Ile	Lys	Arg	Arg	Met	Thr	Asn
225					230					235					240
Asn	Phe	Thr	Lys	Phe	Leu	Gly	Leu	Ile	Ser	Gly	Leu	Ile	Asp	Asp	Arg
			245						250					255	
Leu	Lys	Glu	Arg	Asn	Leu	Arg	Asp	Asn	Ala	Asn	Ile	Asp	Val	Leu	Asp
			260					265					270		
Ala	Leu	Leu	Asn	Ile	Ser	Gln	Glu	Asn	Pro	Glu	Glu	Ile	Asp	Arg	Asn
		275					280					285			
Gln	Ile	Glu	Gln	Leu	Cys	Leu	Asp	Leu	Phe	Ala	Ala	Gly	Thr	Asp	Thr
	290					295					300				
Thr	Ser	Asn	Thr	Leu	Glu	Trp	Ala	Met	Ala	Glu	Leu	Leu	Gln	Asn	Pro
305					310					315					320
His	Thr	Leu	Gln	Lys	Ala	Gln	Glu	Glu	Leu	Ala	Gln	Val	Ile	Gly	Lys
				325					330					335	
Gly	Lys	Gln	Val	Glu	Glu	Ala	Asp	Val	Gly	Arg	Leu	Pro	Tyr	Leu	Arg



180					185					190					
Gly	Ala	Asp	Ala	Asp	His	Lys	Ala	Asp	Glu	Phe	Arg	Ser	Met	Val	Thr
	195						200					205			
Glu	Met	Met	Ala	Leu	Ala	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Val	Pro
	210					215					220				
Ser	Leu	Asp	Trp	Leu	Asp	Leu	Gln	Gly	Val	Ala	Gly	Lys	Met	Lys	Arg
	225					230					235				240
Leu	His	Lys	Arg	Phe	Asp	Ala	Phe	Leu	Ser	Ser	Ile	Leu	Lys	Glu	His
				245					250					255	
Glu	Met	Asn	Gly	Gln	Asp	Gln	Lys	His	Thr	Asp	Met	Leu	Ser	Thr	Leu
			260					265						270	
Ile	Ser	Leu	Lys	Gly	Thr	Asp	Leu	Asp	Gly	Asp	Gly	Gly	Ser	Leu	Thr
			275				280							285	
Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Met	Phe	Thr	Ala	Gly	Thr
	290					295					300				
Asp	Thr	Ser	Ala	Ser	Thr	Val	Asp	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg
	305					310					315				320
His	Pro	Asp	Ile	Met	Val	Lys	Ala	Gln	Glu	Glu	Leu	Asp	Ile	Val	Val
				325					330					335	
Gly	Arg	Asp	Arg	Pro	Val	Asn	Glu	Ser	Asp	Ile	Ala	Gln	Leu	Pro	Tyr
			340					345					350		
Leu	Gln	Ala	Val	Ile	Lys	Glu	Asn	Phe	Arg	Leu	His	Pro	Pro	Thr	Pro
			355				360					365			
Leu	Ser	Leu	Pro	His	Ile	Ala	Ser	Glu	Ser	Cys	Glu	Ile	Asn	Gly	Tyr
	370					375					380				
His	Ile	Pro	Lys	Gly	Ser	Thr	Leu	Leu	Thr	Asn	Ile	Trp	Ala	Ile	Ala
	385					390					395				400
Arg	Asp	Pro	Asp	Gln	Trp	Ser	Asp	Pro	Leu	Ala	Phe	Lys	Pro	Glu	Arg
				405					410					415	
Phe	Leu	Pro	Gly	Gly	Glu	Lys	Ser	Gly	Val	Asp	Val	Lys	Gly	Ser	Asp
			420					425					430		
Phe	Glu	Leu	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Leu
			435				440					445			
Ser	Leu	Gly	Leu	Arg	Thr	Ile	Gln	Phe	Leu	Thr	Ala	Thr	Leu	Val	Gln
	450					455					460				
Gly	Phe	Asp	Trp	Glu	Leu	Ala	Gly	Gly	Val	Thr	Pro	Glu	Lys	Leu	Asn
	465					470					475				480
Met	Glu	Glu	Ser	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Val	Pro	Leu	Val
				485					490					495	

Val His Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser  
500 505 510

Gly

<210> 43  
<211> 7  
<212> PRT  
<213> Arabidopsis thaliana

<400> 43  
Arg Pro Pro Asn Ser Gly Ala  
1 5

<210> 44  
<211> 17  
<212> PRT  
<213> Arabidopsis thaliana

<220>  
<221> UNSURE  
<222> (8)  
<223> Xaa can be any amino acid.

<220>  
<221> UNSURE  
<222> (10)  
<223> Xaa cab be any amino acid.

<220>  
<221> UNSURE  
<222> (15)  
<223> Xaa can be any amino acid.

<400> 44  
Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp  
1 5 10 15

Leu

<210> 45  
<211> 521  
<212> PRT  
<213> Arabidopsis thaliana

<220>  
<221> UNSURE  
<222> (8)  
<223> Xaa can be any amino acid.

<220>  
<221> UNSURE  
<222> (10)  
<223> Xaa cab be any amino acid.

<220>

<221> UNSURE

<222> (15)

<223> Xaa can be any amino acid.

<220>

<221> UNSURE

<222> (18)..(517)

<223> Xaa can be any amino acid. Positions 18-517  
can be 0-500 amino acids.

<400> 45

Arg	Pro	Pro	Asn	Ser	Gly	Ala	Xaa	His	Xaa	Ala	Tyr	Asn	Tyr	Xaa	Asp
1				5					10					15	

Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	50					55					60				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70					75					80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105						110	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		115					120					125			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	130					135					140				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145					150					155					160

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			165						170					175	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			180					185					190		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	195						200					205			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	210					215					220				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
225					230					235					240

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			245						250					255	



Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
260 265 270  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
275 280 285  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
290 295 300  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
305 310 315 320  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
325 330 335  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
340 345 350  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
355 360 365  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
370 375 380  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
385 390 395 400  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
405 410 415  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
420 425 430  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
435 440 445  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
450 455 460  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
465 470 475 480  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
485 490 495  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
500 505 510  
Xaa Xaa Xaa Xaa Xaa Gly Gly Glu Lys  
515 520